



# SEQUENCE LISTING

<110> Grainger, David J.  
Tatalick, Lauen Marie  
Kanaly, Suzanne T.

<120> Compounds and Methods to Inhibit or Augment an Inflammatory Response

<130> 1543.002US1

<140> US 09/150813

<141> 1998-09-11

<150> US 08/927939

<151> 1997-09-11

<160> 111

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 12

<212> PRT

<213> Homo sapiens

<400> 1

Glu Ile Cys Ala Asp Pro Lys Gln Lys Trp Val Gln  
1 5 10

<210> 2

<211> 13

<212> PRT

<213> Homo sapiens

<400> 2

Ala Gln Pro Asp Ala Ile Asn Ala Pro Val Thr Cys Cys  
1 5 10

<210> 3

<211> 15

<212> PRT

<213> Homo sapiens

<400> 3

Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Pro Lys Glu Ala Val  
1 5 10 15

<210> 4

<211> 15

<212> PRT

<213> Homo sapiens

<400> 4

His Leu Lys Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val  
1 5 10 15

<210> 5  
<211> 14  
<212> PRT  
<213> Homo sapiens

<400> 5  
Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val  
1 5 10

<210> 6  
<211> 16  
<212> PRT  
<213> Homo sapiens

<400> 6  
Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr Glu Ile  
1 5 10 15

<210> 7  
<211> 10  
<212> PRT  
<213> Homo sapiens

<400> 7  
Cys Ala Asp Pro Lys Gln Lys Trp Val Gln  
1 5 10

<210> 8  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 8  
Glu Ile Cys Ala Asp Pro  
1 5

<210> 9  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 9  
Lys Gln Lys Trp Val Gln  
1 5

<210> 10  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A synthetic chemokine peptide variant

<400> 10  
Glu Ile Cys Leu Asp Pro Lys Gln Lys Trp Val Gln  
1 5 10

<210> 11  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> A synthetic chemokine peptide variant  
  
 <400> 11  
 Glu Ile Cys Ala Asp Pro Ser Gln Lys Trp Val Gln  
 1 5 10  
  
 <210> 12  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> A synthetic chemokine peptide variant  
  
 <400> 12  
 Glu Ile Cys Ala Asp Pro Ser Glu Glu Trp Val Gln  
 1 5 10  
  
 <210> 13  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> A synthetic chemokine peptide variant  
  
 <400> 13  
 Glu Ile Cys Ala Asp Pro Lys Gln Lys Trp Ile Gln  
 1 5 10  
  
 <210> 14  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> A synthetic chemokine peptide variant  
  
 <400> 14  
 Glu Ile Cys Leu Asp Pro Lys Gln Lys Trp Ile Gln  
 1 5 10  
  
 <210> 15  
 <211> 12  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 15  
 Cys Pro Ser Leu Glu Asp Ser Phe Ile Gln Val Ala  
 1 5 10

<210> 16  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens

<400> 16  
 Met Lys Val Ser Ala Ala Leu Leu Cys Leu Leu Leu Ile Ala Ala Thr  
 1 5 10 15  
 Phe Ile Pro Gln Gly Leu Ala Gln Pro Asp Ala Ile Asn Ala Pro Val  
 20 25 30  
 Thr Cys Cys Tyr Asn Phe Thr Asn Arg Lys Ile Ser Val Gln Arg Leu  
 35 40 45  
 Ala Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Pro Lys Glu Ala Val  
 50 55 60  
 Ile Phe Lys Thr Ile Val Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln  
 65 70 75 80  
 Lys Trp Val Gln Asp Ser Met Asp His Leu Asp Lys Gln Thr Gln Thr  
 85 90 95  
 Pro Lys Thr

<210> 17  
 <211> 77  
 <212> PRT  
 <213> Homo sapiens

<400> 17  
 Ala Gln Pro Asp Ser Val Ser Ile Pro Ile Thr Cys Cys Phe Asn Val  
 1 5 10 15  
 Ile Asn Arg Lys Ile Pro Ile Gln Arg Leu Glu Ser Tyr Thr Arg Ile  
 20 25 30  
 Thr Asn Ile Gln Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Lys Arg  
 35 40 45  
 Gly Lys Glu Val Cys Ala Asp Pro Lys Glu Arg Trp Val Arg Asp Ser  
 50 55 60  
 Met Lys His Leu Asp Gln Ile Phe Gln Asn Leu Lys Pro  
 65 70 75

<210> 18  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens

<400> 18  
 Met Lys Ala Ser Ala Ala Leu Leu Cys Leu Leu Leu Thr Ala Ala Ala  
 1 5 10 15  
 Phe Ser Pro Gln Gly Leu Ala Gln Pro Val Gly Ile Asn Thr Ser Thr  
 20 25 30  
 Thr Cys Cys Tyr Arg Phe Ile Asn Lys Lys Ile Pro Lys Gln Arg Leu  
 35 40 45  
 Glu Ser Tyr Arg Arg Thr Thr Ser Ser His Cys Pro Arg Glu Ala Val  
 50 55 60  
 Ile Phe Lys Thr Lys Leu Asp Lys Glu Ile Cys Ala Asp Pro Thr Gln  
 65 70 75 80  
 Lys Trp Val Gln Asp Phe Met Lys His Leu Asp Lys Lys Thr Gln Thr  
 85 90 95  
 Pro Lys Leu

<210> 19  
 <211> 92  
 <212> PRT  
 <213> Homo sapiens

<400> 19  
 Met Gln Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala  
 1 5 10 15  
 Leu Cys Asn Gln Phe Ser Ala Ser Leu Ala Ala Asp Thr Pro Thr Ala  
 20 25 30  
 Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala  
 35 40 45  
 Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe  
 50 55 60  
 Leu Thr Lys Arg Ser Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp  
 65 70 75 80  
 Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala  
 85 90

<210> 20  
 <211> 92  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
 Met Lys Leu Cys Val Thr Val Leu Ser Leu Leu Met Leu Val Ala Ala  
 1 5 10 15  
 Phe Cys Ser Pro Ala Leu Ser Ala Pro Met Gly Ser Asp Pro Pro Thr  
 20 25 30  
 Ala Cys Cys Phe Ser Tyr Thr Ala Arg Lys Leu Pro Arg Asn Phe Val  
 35 40 45  
 Val Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val  
 50 55 60  
 Phe Gln Thr Lys Arg Ser Lys Gln Val Cys Ala Asp Pro Ser Glu Ser  
 65 70 75 80  
 Trp Val Gln Glu Tyr Val Tyr Asp Leu Glu Leu Asn  
 85 90

<210> 21  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens

<400> 21  
 Met Lys Val Ser Ala Ala Arg Leu Ala Val Ile Leu Ile Ala Thr Ala  
 1 5 10 15  
 Leu Cys Ala Pro Ala Ser Ala Ser Pro Tyr Ser Ser Asp Thr Thr Pro  
 20 25 30  
 Cys Cys Phe Ala Tyr Ile Ala Arg Pro Leu Pro Arg Ala His Ile Lys  
 35 40 45  
 Glu Tyr Phe Tyr Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val Phe  
 50 55 60  
 Val Thr Arg Lys Asn Arg Gln Val Cys Ala Asn Pro Glu Lys Lys Trp  
 65 70 75 80  
 Val Arg Glu Tyr Ile Asn Ser Leu Glu Met Ser  
 85 90

<210> 22  
 <211> 89  
 <212> PRT  
 <213> Homo sapiens

<400> 22  
 Met Asn Ala Lys Val Val Val Val Leu Val Leu Val Leu Thr Ala Leu  
 1 5 10 15  
 Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys  
 20 25 30  
 Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys  
 35 40 45  
 Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys  
 50 55 60  
 Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln  
 65 70 75 80  
 Glu Tyr Leu Glu Lys Ala Leu Asn Lys  
 85

<210> 23  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens

<400> 23  
 Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala Phe Leu Ile Ser  
 1 5 10 15  
 Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser Ala Lys Glu Leu  
 20 25 30  
 Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His Pro Lys Phe  
 35 40 45  
 Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr  
 50 55 60  
 Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu Cys Leu Asp Pro  
 65 70 75 80  
 Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys Phe Leu Lys Arg Ala  
 85 90 95  
 Glu Asn Ser

<210> 24  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens

<400> 24  
 Met Ala Arg Ala Ala Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu  
 1 5 10 15  
 Arg Val Ala Leu Leu Leu Leu Leu Val Ala Ala Gly Arg Arg Ala  
 20 25 30  
 Ala Gly Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr  
 35 40 45  
 Leu Gln Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val Lys Ser  
 50 55 60  
 Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn  
 65 70 75 80  
 Gly Arg Lys Ala Cys Leu Asn Pro Ala Ser Pro Ile Val Lys Lys Ile  
 85 90 95  
 Ile Glu Lys Met Leu Asn Ser Asp Lys Ser Asn  
 100 105

<210> 25  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens

<400> 25  
 Met Lys Val Ser Ala Ala Leu Leu Trp Leu Leu Leu Ile Ala Ala Ala  
 1 5 10 15  
 Phe Ser Pro Gln Gly Leu Ala Gly Pro Ala Ser Val Pro Thr Thr Cys  
 20 25 30  
 Cys Phe Asn Leu Ala Asn Arg Lys Ile Pro Leu Gln Arg Leu Glu Ser  
 35 40 45  
 Tyr Arg Arg Ile Thr Ser Gly Lys Cys Pro Gln Lys Ala Val Ile Phe  
 50 55 60  
 Lys Thr Lys Leu Ala Lys Asp Ile Cys Ala Asp Pro Lys Lys Lys Trp  
 65 70 75 80  
 Val Gln Asp Ser Met Lys Tyr Leu Asp Gln Lys Ser Pro Thr Pro Lys  
 85 90 95  
 Pro

<210> 26  
 <211> 148  
 <212> PRT  
 <213> Mus musculus

<400> 26  
 Met Gln Val Pro Val Met Leu Leu Gly Leu Leu Phe Thr Val Ala Gly  
 1 5 10 15  
 Trp Ser Ile His Val Leu Ala Gln Pro Asp Ala Val Asn Ala Pro Leu  
 20 25 30  
 Thr Cys Cys Tyr Ser Phe Thr Ser Lys Met Ile Pro Met Ser Arg Leu  
 35 40 45  
 Glu Ser Tyr Lys Arg Ile Thr Ser Ser Arg Cys Pro Lys Glu Ala Val  
 50 55 60  
 Val Phe Val Thr Lys Leu Lys Arg Glu Val Cys Ala Asp Pro Lys Lys  
 65 70 75 80  
 Glu Trp Val Gln Thr Tyr Ile Lys Asn Leu Asp Arg Asn Gln Met Arg  
 85 90 95  
 Ser Glu Pro Thr Thr Leu Phe Lys Thr Ala Ser Ala Leu Arg Ser Ser  
 100 105 110  
 Ala Pro Leu Asn Val Lys Leu Thr Arg Lys Ser Glu Ala Asn Ala Ser  
 115 120 125  
 Thr Thr Phe Ser Thr Thr Thr Ser Ser Thr Ser Val Gly Val Thr Ser  
 130 135 140  
 Val Thr Val Asn  
 145

<210> 27  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A synthetic chemokine peptide variant

<400> 27  
 Cys Leu Asp Pro Lys Lys Glu Trp Ile Gln  
 1 5 10

```
<220>  
<221> CDS  
<222> (34) ... (327)
```

ctg tgc ctg ctg ctc atg aca gca gct ttc aac ccc cag gga ctt gct 102  
Leu Cys Leu Leu Leu Met Thr Ala Ala Phe Asn Pro Gln Gly Leu Ala  
10 15 20

cag cca gat gca ctc aac gtc cca tct act tgc tgc ttc aca ttt agc 150  
Gln Pro Asp Ala Leu Asn Val Pro Ser Thr Cys Cys Phe Thr Phe Ser  
25 30 35

agt aag aag atc tcc ttg cag agg ctg aag agc tat gtg atc acc acc 198  
 Ser Lys Lys Ile Ser Leu Gln Arg Leu Lys Ser Tyr Val Ile Thr Thr  
 40 45 50 55

agc agg tgt ccc cag aag gct gtc atc ttc aga acc aaa ctg ggc aag 246  
Ser Arg Cys Pro Gln Lys Ala Val Ile Phe Arg Thr Lys Leu Gly Lys  
60 65 70

gag atc tgt gct gac cca aag gag aag tgg gtc cag aat tat atg aaa 294  
Glu Ile Cys Ala Asp Pro Lys Glu Lys Trp Val Gln Asn Tyr Met Lys  
75 80 85

cac ctg ggc cgg aaa gct cac acc ctg aag act tgaactctgc taccctact 347  
 His Leu Gly Arg Lys Ala His Thr Leu Lys Thr  
 90 95

gaaatcaagc	tggagtagt	gaaatgactt	tccattctc	ctctggcctc	ctcttctatg	407
ctttggaata	cttctaccat	aattttcaaa	taggatgcat	tcggttttgt	gattcaaaat	467
gtactatgtg	ttaagtaata	ttggctatta	tttgacttgt	tgctggtttg	gagtttattt	527
gagtattgct	gatcttttct	aaagcaaggc	cttgagcaag	taggttgctg	tctctaagcc	587
cccttccctt	ccactatgag	ctgctggcag	tgggttgtat	tcggttccca	ggggttgaga	647
gcatgcctgt	gggagtcag	gacatgaagg	gatctgcaa	tgtaggaagg	agagctcttt	707
gtgaatgtga	gggtgttgct	aaattattgt	tattgtgga	aagatgaatg	caatagtagg	767
actgctgaca	ttttgcagaa	aatacatttt	atttaaaatc	tcctaaaaaa	aaaaaaaa	825

```
<210> 29
<211> 3524
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> (80) ... (358)
```

```

<400> 29
tctccgtcag ccgcattgcc cgctcggcgt ccggcccccg acccgtgctc gtccgcccgc 60
ccgcccgcgc gccgcgcgc atg aac gcc aag gtc gtg gtc gtg ctg gtc ctc 112
          Met Asn Ala Lys Val Val Val Val Leu Val Leu
                1                5                10

```



gtg	ctg	acc	gcg	ctc	tgc	ctc	agc	gac	ggg	aag	ccc	gtc	agc	ctg	agc	160
Val	Leu	Thr	Ala	Leu	Cys	Leu	Ser	Asp	Gly	Lys	Pro	Val	Ser	Leu	Ser	
			15					20					25			
tac	aga	tgc	cca	tgc	cga	ttc	ttc	gaa	agc	cat	gtt	gcc	aga	gcc	aac	208
Tyr	Arg	Cys	Pro	Cys	Arg	Phe	Phe	Glu	Ser	His	Val	Ala	Arg	Ala	Asn	
		30				35						40				
gtc	aag	cat	ctc	aaa	att	ctc	aac	act	cca	aac	tgt	gcc	ctt	cag	att	256
Val	Lys	His	Leu	Lys	Ile	Leu	Asn	Thr	Pro	Asn	Cys	Ala	Leu	Gln	Ile	
	45					50					55					
gta	gcc	cgg	ctg	aag	aac	aac	aac	aga	caa	gtg	tgc	att	gac	ccg	aag	304
Val	Ala	Arg	Leu	Lys	Asn	Asn	Asn	Arg	Gln	Val	Cys	Ile	Asp	Pro	Lys	
	60				65				70						75	
cta	aag	tgg	att	cag	gag	tac	ctg	gag	aaa	gct	tta	aac	aag	agg	ttc	352
Leu	Lys	Trp	Ile	Gln	Glu	Tyr	Leu	Glu	Lys	Ala	Leu	Asn	Lys	Arg	Phe	
			80						85					90		
aag	atg	tgagaggggc	agacgcctga	ggaaccctta	cagtaggagc	ccagctctga	408									
Lys	Met															

aaccagtgtt	aggggaagggc	ctgccacagc	ctccccctgcc	agggcagggc	cccaggcatt	468
gccaagggct	ttgttttgca	cactttgcca	tattttcacc	atttgattat	gtagcaaaat	528
acatgacatt	tatttttcat	ttagtttgat	tattcagtgt	cactggcgac	acgtagcagc	588
ttagactaag	gccattattg	tacttgccct	attagagtgt	ctttccacgg	agccactcct	648
ctgactcagg	gctcctgggt	tttgatttct	ctgagctgtg	caggtgggga	gactgggctg	708
agggagcctg	gccccatggg	cagccctagg	gtggagagcc	accaagaggg	acgcctgggg	768
gtgccaggac	cagtcaacct	gggcaaagcc	tagtgaaggc	ttctctctgt	gggatgggat	828
gggtggagggc	cacatggggag	gctcaccccc	ttctccatcc	acatggggagc	cgggtctgcc	888
tcttctggga	gggcagcagg	gctaccctga	gctgaggcag	cagtgtgagg	ccagggcaga	948
gtgagaccca	gcctcatcc	cgagcacctc	cacatcctcc	acgttctgct	catcattctc	1008
tgtctcatcc	atcatcatgt	gtgtccacga	ctgtctccat	ggccccgcaa	aaggactctc	1068
aggaccaaag	ctttcatgta	aactgtgcac	caagcaggaa	atgaaaatgt	cttgtgttac	1128
ctgaaaacac	tgtgcacatc	tgtgtcttgt	gtggaatatt	gtccattgtc	caatcctatg	1188
ttttgtttca	aagccagcgt	cctcctctgt	gaccaatgtc	ttgatgcatg	cactgtttcc	1248
cctgtgcagc	cgctgagcga	ggagatgctc	cttgggccct	ttgagtgcag	tcctgatcag	1308
agccgtggtc	ctttgggggtg	aactaccttg	gttccccccac	tgatcacaaa	aacatgggtgg	1368
gtccatgggc	agagcccaag	ggaattcggg	gtgcaccagg	gttgacccca	gaggattgct	1428
gccccatcag	tgctccctca	catgtcagta	ccttcaaact	agggccaagc	ccagcactgc	1488
ttgaggaaaa	caagcattca	caacttgttt	ttggttttta	aaacccagtc	cacaaaaata	1548
ccaatcctgg	acatgaagat	tctttcccaa	ttcacatcta	acctcatctt	cttcaccatt	1608
tggcaatgcc	atcatctcct	gccttcctcc	tgggccctct	ctgctctgcg	tgacacctgt	1668
gcttcggggc	cttcccacag	gacatttctc	taagagaaca	atgtgctatg	tgaagagtaa	1728
gtcaacctgc	ctgacatttg	gagtgttccc	ctcccactga	gggcagtcga	tagagctgta	1788
ttaagccact	taaaatgttc	acttttgaca	aaggcaagca	cttgtgggtt	tttgttttgt	1848
ttttcattca	gtcttacgaa	tacttttgcc	ctttgattaa	agactccagt	taaaaaaaaat	1908
tttaatgaag	aaagtggaaa	acaaggaagt	caaagcaagg	aaactatgta	acatgtagga	1968
agtaggaagt	aaattatagt	gatgtaatct	tgaattgtaa	ctgttcgtga	atttaataat	2028
ctgtagggta	attagtaaca	tgtgttaagt	attttcataa	gtattttcaa	ttggagcttc	2088
atggcagaag	gcaaacccat	caacaaaaat	tgtcccttaa	acaaaaatta	aaatcctcaa	2148
tccagctatg	ttatatgaa	aaaatagagc	ctgagggatc	tttactagtt	ataaagatac	2208
agaactcttt	caaaaccttt	tgaaattaac	ctctcactat	accagtataa	ttgagttttc	2268
agtggggcag	tcattatcca	ggtaatccaa	gatattttta	aatctgtcac	gtagaacttg	2328
gatgtacctg	cccccaatcc	atgaaccaag	accattgaat	tcttggttga	ggaaacaaac	2388
atgaccctaa	atcttgacta	cagtcaggaa	aggaatcatt	tctattttctc	ctccatggga	2448
gaaaatagat	aagagtagaa	actgcaggga	aaattatttg	cataacaatt	cctctactaa	2508
caatcagctc	cttcctggag	actgccagc	taaagcaata	tgcattttaa	tacagtcttc	2568
catttgcaag	ggaaaagtct	cttgtaatcc	gaatctcttt	ttgctttcga	actgctagtc	2628

aagtgcgtcc	acgagctggt	tactagggat	ccctcatctg	tccctccggg	acctgggtgct	2688
gcctctacct	gacactccct	tgggctccct	gtaacctctt	cagaggccct	cgctgccagc	2748
tctgtatcag	gacccagagg	aaggggccag	aggctcgttg	actggctgtg	tggtgggatt	2808
gagtcgtgag	cacgtgtatg	tgctgtgggt	tgtccccctc	tgtccaggca	ctgagatacc	2868
agcgaggagg	ctccagaggg	cactctgctt	gttattagag	attacctcct	gagaaaaaag	2928
cttccgcttg	gagcagaggg	gctgaatagc	agaagggtgc	acctccccca	accttagatg	2988
ttctaagtct	ttccattgga	tctcattgga	cccttccatg	gtgtgatcgt	ctgactgggtg	3048
ttatcaccgt	gggctccctg	actgggagtt	gatcgccctt	cccagggtgct	acaccctttt	3108
ccagctggat	gagaatttga	gtgctctgat	ccctctacag	agcttccctg	actcattctg	3168
aaggagcccc	attcctggga	aatattccct	agaaacttcc	aaatccccta	agcagaccac	3228
tgataaaacc	atgtagaaaa	tttgttatct	tgcaacctcg	ctggactctc	agtctctgag	3288
cagtgaatga	ttcagtggtta	aatgtgatga	atactgtatt	ttgtattggt	tcaagtgcac	3348
ctcccagata	atgtgaaaaat	ggtcaggag	aaggccaatt	cctatacgca	gcgtgcttta	3408
aaaaataaat	aagaaacaac	tctttgagaa	acaacaattt	ctactttgaa	gtcataccaa	3468
tgaaaaaatg	tatatgcact	tataattttc	ctaataaagt	tctgtactca	aatgta	3524

<210> 30

<211> 4259

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (2070) ... (2130)

<220>

<221> CDS

<222> (2669) ... (2795)

<220>

<221> CDS

<222> (2990) ... (3079)

<220>

<221> CDS

<222> (3491) ... (3506)

<400> 30

gaattcggag	gtctacctgc	ctctgcctcc	caagtactgg	aattactctt	acggcttact	60
tttcctcaag	gggtcttcaa	gcactttctga	ccatagggag	cggactctta	ggaaattcca	120
tatagattct	tttatttcag	tcatttgaca	ttacttttat	agtcataaat	tttgatattt	180
ttttacagat	ctgaatatgt	ttgaagaaat	gttcattttt	cccctagcca	caaaaaatccc	240
atgacatgta	taccatactt	gccataacct	gctataattc	agtgcataat	ggcctgttct	300
agtcaaaagg	ctgctttcaa	gtacgagtga	ctattttactg	gatacaaatgt	atgtatacta	360
cagtaacttt	catttttagca	tgaaattctg	tgtaaaacaa	gtccaattta	aaccccttct	420
agggtgttag	ttccagaaac	accaagaaa	catcaaagat	aacttcagcc	aagcagacac	480
aggcaagtct	ggagcctgaa	ccaaggatct	gctctttgga	gacactgcat	aaccaagtgt	540
ttgagagcgt	gggctacaga	gatggagttt	ctggattcct	agaggggtga	atgagggaaa	600
actcttgact	aacagatgct	taacactacg	caatagttag	taaactcttt	tctcctcagt	660
aagggactat	atatccactt	gctaactgtt	ttttcttaac	atcctcaaat	ctgtttttcc	720
ttcacatctt	gactgagaac	ttgtacaata	acaaaataaa	ataaaaactgt	caccatgtat	780
ctttctttat	tgtttaatat	aaaactgctc	agcacctctt	tccactctaa	aattctgagg	840
ttcctacagc	gcagcgtcta	ttctgcagaa	gcaggttggg	agagactgct	catggcgtcc	900
tctcacagta	gccttctccc	agcagaagg	tgcaaaacga	aagtctcttg	gcttgtctct	960
gcccccatc	ccttctgtct	gtccttccag	attccacggc	tgtcccgtag	tttgtctcct	1020
tgaaaagctta	gctctgttct	agtccttgga	ctacatcaat	gtggattttg	ctctctagaa	1080
atttctatct	ttcccaagca	gcaactccct	tcctgttctg	gtgacagctc	ctgtttccca	1140
gttcccatg	gtgggttagag	gtttcactct	tgccctctgt	tgtcaagttt	tgaaccggta	1200
cactccaggc	tcctgtccca	ttcccaggat	gagtcacctc	catccctctc	atcactgtca	1260
cctctatgag	agatctatgt	aacctcacct	actcttccag	gtcccaggta	tctgctgcct	1320
tgggtgctct	gcagagtga	atccacattc	actttcatcc	ttgaccctgt	taccacacac	1380
tcacaaagaa	gacaatcaaa	gcatccctga	gagaatcagc	acggggcaac	aattagcttt	1440

gcaattcctc	ttgtaacttg	taaacattag	tgtgacactt	cgggcttctg	ttctgaatgc	1500
ctgctctaac	tgttcactaa	gttgtataga	ctttggatct	ggctaaattt	ggcatgtgat	1560
ttttttttta	aagtttattc	caagtatttt	ataataaagc	ctatgaagta	aaaagcaaaa	1620
ataaacagtg	taaacacaa	aaatgtaaaa	accatggtta	gaacctgact	tagatatcag	1680
ctctgtgttt	tatttatgag	agaaggaaga	tgagaattaa	agccatttcc	agacttattc	1740
tgcaaggcac	tcattctgatt	tctcaaacag	ctcacgcttt	ggaaagtga	acctacctca	1800
ctcgttaaaa	attaaaagga	gcacaagagg	ggagagggaa	attccaagtt	catgggtcac	1860
aataaacaca	agcaatgccc	tcggtttaca	ggggacttcc	ctcgggttgc	ggagccttgc	1920
tgagtcattc	ccaaagtcag	ccaatcagga	ctcagggagg	gaaactcttt	gcagataaat	1980
actcctcagc	agccggcact	cgagaagcgc	ttcatccacc	gctgagagac	atcccagacc	2040
aaccttcagg	aagcctcccc	atcagcacc	atg aac cca	agt gct gcc gtc att		2093

Met	Asn	Pro	Ser	Ala	Ala	Val	Ile
1			5				

ttc tgc ctc atc ctg ctg ggt ctg agt ggg act	caa g gtaagggaca	2140
Phe Cys Leu Ile Leu Leu Gly Leu Ser Gly Thr	Gln	
10	15	20

ccaaggccat	ttaattaacg	aagtcagaag	tcagacgatt	aagctcagtt	ctaaacacag	2200
catgtattta	agctttaatg	tgtgtacct	ttaaagaagag	ggaagcagga	agaaatccct	2260
tcagcttgca	gagtttatca	taggctgggt	gaagtcagag	aaaaatagaa	taaaagaaaa	2320
ggaacgaaga	aggggaagaaa	gggagaaaa	gaggagggag	gaggaagaag	gagggagag	2380
agagtcagga	gaaagggcga	aagagtggga	tggggtaagg	catggatgcc	tccttgcttg	2440
agcctaacca	atactgtgag	cagtgcataa	atgcaggatt	tcgtaactga	caagttgcag	2500
atctctcttt	accatgacca	agatattcaa	acactcagcc	ctatgatacg	atgggatgcg	2560
tctctccaca	gatcagacag	ggtctgctaa	acactacctc	atccatttta	agtgccctaaa	2620
atgaaaccgt	gtgctgacct	tcctggctct	ccccctctct	tcctgcag gg atc cct		2676

Gly Ile Pro

ctc gca agg acg gtc cgc tgc aac tgc atc cat	atc gat gac ggg cca	2724
Leu Ala Arg Thr Val Arg Cys Asn Cys Ile His	Ile Asp Asp Gly Pro	
25	30	35

gtg aga atg agg gcc ata ggg aag ctt gaa atc	atc cct gcg agc cta	2772
Val Arg Met Arg Ala Ile Gly Lys Leu Glu Ile	Ile Pro Ala Ser Leu	
40	45	50

tcc tgc cca cgt gtt gag atc at gtgagtacaa	gcccacctgc cgataaacgt	2825
Ser Cys Pro Arg Val Glu Ile Ile		
60		

ccctcccgta	accacacagt	aaataagtga	gggaaaccag	gaaagatggg	gacgggtctg	2885
tgactctaac	taaggcacag	tgacctgaact	ctgacatgga	cctgcagggc	catcagctct	2945
gttggcctga	cgtaaatctg	agtatctcac	tcttatttct	atag t gcc acg atg		2999

Ala Thr Met  
65

aaa aag aat gat gag cag aga tgt ctg aat ccg	gaa tct aag acc atc	3047
Lys Lys Asn Asp Glu Gln Arg Cys Leu Asn Pro	Glu Ser Lys Thr Ile	
70	75	80

aag aat tta atg aaa gcg ttt agc caa aaa ag	gtaggtttga tggttgctttt	3099
Lys Asn Leu Met Lys Ala Phe Ser Gln Lys Arg		
85	90	

tcaggaaatg	gtgggtctggg	gagcagcgcc	tgccctgggc	tttgctgtgg	gcatctgccc	3159
taaactcatg	gcaccggcat	gtgcctttgt	ctctccattt	acacagacac	tgaggtgcct	3219
tcttaggtca	tacattccta	gtgtctagaa	gtggagcagt	tattatacct	gtcacgggta	3279
aagctgccaa	atgcccaccc	ccccacttcc	tactttaaaa	aaaaaaaaacc	aaaaacaaac	3339
aaacccattc	tgtccctcca	acccccaccc	acccgtgacc	catggagatt	gtgtagcaga	3399
ggaaaaatgca	ccaggccttt	tgccccaggg	tctttgggtt	ccaaagtga	agcagagtct	3459

```

atccgctcaa tacagtttcc tcttccctaca g g tct aaa agg gct cct      3506
                               Ser Lys Arg Ala Pro
                               95

taactggaga gaagccacgc acacaccccg gtgctgtgat ggacagcaga gagcctgtct 3566
ctccatcact cccctttacc cagtggatgg ctagtcctaa ttgcccttgg tcttctgaaa 3626
ggtgaccagc cgtggtcaca tcagctgcta ctctctctgc aggatgatgg ttaagccatg 3686
gtcctgagac aaaagtaact gccgaagcaa gaattcttta agggctggtc tgagtcctca 3746
ctcaagtggc tgggatggct gtcctagctc tgtactgtaa gctatgtgga ggtgcgacgc 3806
ccttcaccat gtgccacgcc ccaggctgct cccacacccc tccttgtcct ccctagctca 3866
ggctcgtcag ttctgagttt acctgagctc ttttatttca gatgtaagac tacaaattta 3926
agtttgtaag gacaaactta accaccatct tcccaagggg ttatcaagat actcagagga 3986
acctggaaat gtatgtgtaa atactattta atgaacgact gtacaaagta gaattcctag 4046
atgtattttt tgtatgcttt gcattgtata tggagaact tgtgtcatca agtatgtatc 4106
aatgggtagt taaagtttat ttttaaaacc gtccaatacc ttttgtatta tgtaacattc 4166
aaaagacaat gtactgtatt gaaagtagta agagacccaa aatgtaataa agtaataata 4226
actgacatga aatggtcatg tgactgagaa ttc                                4259

<210> 31
<211> 1081
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (43)...(363)

<400> 31
ctctcctcct cgcacagccg ctccaaccgc ctgctgagcc cc atg gcc cgc gcc      54
                               Met Ala Arg Ala
                               1

acg ctc tcc gcc gcc ccc agc aat ccc cgg ctc ctg cgg gtg gcg ctg      102
Thr Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu Arg Val Ala Leu
 5                               10                               15                               20

ctg ctc ctg ctc ctg gtg gcc gcc agc cgg cgc gca gca gga gcg ccc      150
Leu Leu Leu Leu Val Ala Ala Ser Arg Arg Ala Ala Gly Ala Pro
 25                               30                               35

ctg gcc act gaa ctg cgc tgc cag tgc ttg cag acc ctg cag gga att      198
Leu Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr Leu Gln Gly Ile
 40                               45                               50

cac ctc aag aac atc caa agt gtg aag gtg aag tcc ccc gga ccc cac      246
His Leu Lys Asn Ile Gln Ser Val Lys Val Lys Ser Pro Gly Pro His
 55                               60                               65

tgc gcc caa acc gaa gtc ata gcc aca ctc aag aat ggg cag aaa gct      294
Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn Gly Gln Lys Ala
 70                               75                               80

tgt ctc aac ccc gca tcg ccc atg gtt aag aaa atc atc gaa aag atg      342
Cys Leu Asn Pro Ala Ser Pro Met Val Lys Lys Ile Ile Glu Lys Met
 85                               90                               95                               100

ctg aaa aat ggc aaa tcc aac tgaccagaag gaaggaggaa gcttattggt      393
Leu Lys Asn Gly Lys Ser Asn
 105

ggctgttcct gaaggaggcc ctgcccttac aggaacagaa gaggaaagag agacacagct 453
gcagaggcca cctggattgc gcctaattgtg tttgagcatc acttaggaga agtcttctat 513

```

ttattttattt	atattttat	ttgtttgttt	tagaagattc	tatgttaata	ttttatgtgt	573
aaaataaggt	tatgattgaa	tctacttgca	cactctccca	ttatatttat	tgttttatttt	633
agggtcaaacc	caagtttagtt	caatcctgat	tcatatttaa	tttgaagata	gaagggttgc	693
agatattctc	tagtcatttg	ttaatatattc	ttcgtgatga	catatcacat	gtcagccact	753
gtgatagagg	ctgaggaatc	caagaaaatg	gccagtgaga	tcaatgtgac	ggcagggaaa	813
tgtatgtgtg	tctattttgt	aactgtaaag	atgaatgtca	gttgttattt	attgaaatga	873
tttcacagtg	tgtgggtcaac	atcttctcatg	ttgaagcttt	aagaactaaa	atgttctaaa	933
tatcccttgg	acattttatg	tctttcttgt	aaggcatact	gccttgttta	atgttaatta	993
tgcagtgttt	ccctctgtgt	tagagcagag	aggtttcgat	atttattgat	gttttcacaa	1053
agaacaggaa	aataaaaatat	ttaaaaaat				1081

<210> 32

<211> 1173

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (107) ... (448)

<400> 32

cggcagcagc	acagtgtctc	ggatcctcca	atcttcgctc	ctccaatctc	cgctcctcca	60
cccagttcag	gaaccgcgca	cgcctcgcag	cgctctcttg	accact	atg agc ctc	115
					Met Ser Leu	
					1	

ctg	tcc	agc	cgc	gcg	gcc	cgt	gtc	ccc	ggg	cct	tcg	agc	tcc	ttg	tgc	163
Leu	Ser	Ser	Arg	Ala	Ala	Arg	Val	Pro	Gly	Pro	Ser	Ser	Ser	Leu	Cys	
	5					10					15					

gcg	ctg	ttg	gtg	ctg	ctg	ctg	ctg	ctg	acg	cag	cca	ggg	ccc	atc	gcc	211
Ala	Leu	Leu	Val	Leu	Leu	Leu	Leu	Leu	Thr	Gln	Pro	Gly	Pro	Ile	Ala	
	20				25					30					35	

agc	gct	ggg	cct	gcc	gct	gct	gtg	ttg	aga	gag	ctg	cgt	tgc	gtt	tgt	259
Ser	Ala	Gly	Pro	Ala	Ala	Ala	Val	Leu	Arg	Glu	Leu	Arg	Cys	Val	Cys	
				40					45					50		

tta	cag	acc	acg	cag	gga	gtt	cat	ccc	aaa	atg	atc	agt	aat	ctg	caa	307
Leu	Gln	Thr	Thr	Gln	Gly	Val	His	Pro	Lys	Met	Ile	Ser	Asn	Leu	Gln	
			55					60					65			

gtg	ttc	gcc	ata	ggc	cca	cag	tgc	tcc	aag	gtg	gaa	gtg	gta	gcc	tcc	355
Val	Phe	Ala	Ile	Gly	Pro	Gln	Cys	Ser	Lys	Val	Glu	Val	Val	Ala	Ser	
		70					75					80				

ctg	aag	aac	ggg	aag	gaa	att	tgt	ctt	gat	cca	gaa	gcc	cct	ttt	cta	403
Leu	Lys	Asn	Gly	Lys	Glu	Ile	Cys	Leu	Asp	Pro	Glu	Ala	Pro	Phe	Leu	
	85					90					95					

aag	aaa	gtc	atc	cag	aaa	att	ttg	gac	ggg	gga	aac	aag	gaa	aac		448
Lys	Lys	Val	Ile	Gln	Lys	Ile	Leu	Asp	Gly	Gly	Asn	Lys	Glu	Asn		
100					105					110						

tgattaagag	aaatgagcac	gcatggaaaa	gtttcccagt	ctacagcaga	gaagttttct	508
ggagggtctct	gaacccaggg	aagacaagaa	ggaaagattt	tggtgtgtgt	tgtttatttg	568
gtttccccag	tagtttagctt	tcttccctgg	attcctcact	tttgaagagt	gtgaggaaaa	628
cctatgtttg	gcgcttaagc	tttcagctca	gcttaatgaa	gtgttttagca	tagtacctct	688
gctattttgct	gttattttat	ctgctatgct	attgaagttt	tggcaattga	ctatagtgtg	748
agccaggaat	cactggctgt	taatcttaca	aagtgtcttg	gaattgtagg	tgactattat	808
ttttccaaga	aataaccctt	aagatattaa	ctgagaaggc	tgggggttta	atgtggaaat	868
gatgtttcaa	aaggaatcct	gtgatggaaa	tacaactggg	atcttcactt	tttttaggaat	928

```
<220>
<221> CDS
<222> (1192) ... (1267)
```

<220>  
 <221> CDS  
 <222> (1953) ... (2067)

<220>  
 <221> CDS  
 <222> (2488) ... (2575)

<400> 34  
 ttagagactt aataataaag gatcttgttg ataatttatac attccctgat agagaaaaat 60  
 ttagctttgc ttatttttaga gttataaatg atgctgggtc aggtatcttt atgtttgaag 120  
 atggctccat atttgggttg tttccacaga actctttccc agaaatgctt tttctagggtt 180  
 aatggctaca catatttcta ggcacctgac atactgacac ccacctctaa agtattttta 240  
 tgatccacaa ctagecgttta acacagcgcc ccagtcactc cgagactaat aaatagacaa 300  
 atgactgaaa cgtgacctca tgctttctat tccctccagct ttcattgagt tcccttcctc 360  
 tgggaggact ggggggttgct tagccctcca cagcatcagc ccattgacct tatccttggtg 420  
 gttatagcag ctgaggaagc agaattacag ctctgtggga aggaatgggg ctggagaggtt 480  
 catgcataga ccaattcttt tttttttttt ttttttgagat ggagtttcac ttttggtgcc 540  
 caggctggag tgcaatggca tgatctcagc tcaccacagc cccacacctc tgggttcaag 600  
 cgattctcct gccctcagcc tcccagtag ctgggattac aggcattgtc caccacgcct 660  
 gactactttt gtatttttag tagagatgga gtttctcttt cttggtcagg ttggtctcaa 720  
 actcctgacc tcagggtgatc cgcagcctcg gcctcccaaa gtgttgggat tacagggtgtg 780  
 agcgaccatg cctggctgca tagaccagtt cttatgagaa gggatcaact aagaatagcc 840  
 ttgggttgac acacacccct cttcacactc acaggagaaa ccccatgaag ctagaaccag 900  
 tcatgagttg agagctgaga gtttagagagt agctcagaga tgctattctt ggatatcctg 960  
 agcccctgtg gtcaccaggg accctgagtt gtgcaacact cagcatgaca gcatcactac 1020  
 acttaaaaat ttccctcctc acccccagat tccatttccc catccgccag ggctgcctat 1080  
 aaagaggaga gatggcttca gacatcagaa ggacgcaggc agcaaagagt agtcagtcctc 1140  
 ttcttggctc tgctgacact cgagcccaca ttccatcacc tgctcccaat c atg cag 1197  
 Met Gln  
 1

gtc tcc act gct gcc ctt gcc gtc ctc ctc tgc acc atg gct ctc tgc 1245  
 Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala Leu Cys  
 5 10 15

aac cag gtc ctc tct gca cca c gtgagtccat gttgttgttg tgggtatcac 1297  
 Asn Gln Val Leu Ser Ala Pro  
 20 25

cactctctgg ccatgggttag accacatcag tcttttttttg cggcctgaga gccccgaaga 1357  
 gaaaagaagg aagtctctaa agcgtgcca aacaccttgg tctttttctt cacaactttt 1417  
 atttttatct ctagaagggg tcttagccct cctagtctcc aggtatgaga atctaggcag 1477  
 gggcagggga gttacagtcc cttgtacaga tagaaaaaca ggggttcaaaa cgaatcagtt 1537  
 tgcaagaggc agaatccagg gctgcttact tcccagtggt gtctgttgtt cactctccag 1597  
 ctcaccctag gtctcccagg agccctgtcc cttggatgtc ttatgagaga tgtccagggc 1657  
 ttctcttggg ctgggggtatg acttcttgaa ccgacaaaat tccatgaaga gagctaagag 1717  
 aacagtccat tcagggtatct ggatcacata gagaaacaga gaaccacta tgaagagtca 1777  
 aggggaaaga ggaatataga cagaaacaaa gagacatttc tctgcaaaac cccccaaatg 1837  
 ccttgcagtc acttgggtctg agcaagcctg ccctcctcaa ccactcaggg atcagaagct 1897  
 gcctggcctt ttcttctgag ctgtgactcg ggcttattct ctcctttctc cgcag tt 1954  
 Leu

gct gct gac acg ccg acc gcc tgc tgc ttc agc tac acc tcc cga cag 2002  
 Ala Ala Asp Thr Pro Thr Ala Cys Cys Phe Ser Tyr Thr Ser Arg Gln  
 30 35 40

att cca cag aat ttc ata gct gac tac ttt gag acg agc agc cag tgc 2050  
 Ile Pro Gln Asn Phe Ile Ala Asp Tyr Phe Glu Thr Ser Ser Gln Cys  
 45 50 55

tcc aag ccc agt gtc at gtaagtgccca gtcttctctgc tcacctctag 2097  
 Ser Lys Pro Ser Val Ile  
 60

ggaggtaggg agtgtcaggg tgggggcaga aacaggccag aaggccatcc tggaaaggcc 2157  
 cagccttcag gaggctatcg gggatacagg acgcaggcca ctgaggtgtg acctgacttg 2217  
 gggctggagt gaggtgggtg ttacagagtc aggaagggtc gcccaggcc agaggaaagg 2277  
 aacaggaaga aggaggcagc aggacactct gagggccccc ttgcctggag tcaactgagag 2337  
 aagctctcta gacggagata ggcagggggc ccctgagaga ggagcaggcc ttgagctgcc 2397  
 caggacagag agcaggatgt caggccatgg tgggcccagg attccccggc tggattcccc 2457  
 agtgcttaac tcttctctccc ttctccacag c ttc cta acc aag aga ggc cgg 2509  
 Phe Leu Thr Lys Arg Gly Arg  
 65 70

cag gtc tgt gct gac ccc agt gag gag tgg gtc cag aaa tac gtc agt 2557  
 Gln Val Cys Ala Asp Pro Ser Glu Glu Trp Val Gln Lys Tyr Val Ser  
 75 80 85

gac ctg gag ctg agt gcc tgaggggtcc agaagcttcg aggcccagcg 2605  
 Asp Leu Glu Leu Ser Ala  
 90

acctcagtgg 'gccagtgagg gagggagcagg agcctgagcc ttgggaacat gcgtgtgacc 2665  
 tctacagcta cctcttctat ggactgggta ttgccaaaca gccacactgt gggactcttc 2725  
 ttaacttaaa ttttaattta ttataactat ttagttttta taattttatt ttgatttcac 2785  
 agtgtgtttg tgattgtttg ctctgagagt tccccctgtc ccctccacct tccctcacag 2845  
 tgtgtctggt gacgaccgag tggctgtcat cggcctgtgt aggcagtcac ggcaccaaag 2905  
 ccaccagact gacaaatgtg tatcagatgc ttttgttcag ggctgtgatc ggcctgggga 2965  
 aataataaag atgttctttt aaacggtaaa ccagtattga gtttggtttt gtttttcttg 3025  
 caaatcaaaa tcaactagta agaggaatca taggcaaaga ttaggaagag gtgaaatgga 3085  
 gggaaactgg gagagatggg gagcgct 3112

<210> 35  
 <211> 481  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (55)...(333)

<400> 35  
 agcctctgaa gctcccacca ggccagctct cctcccacaa cagcttccca cagc atg 57  
 Met  
 1

aag atc tcc gtg gct gcc att ccc ttc ttc ctc ctc atc acc atc gcc 105  
 Lys Ile Ser Val Ala Ala Ile Pro Phe Phe Leu Leu Ile Thr Ile Ala  
 5 10 15

cta ggg acc aag act gaa tcc tcc tca cgg gga cct tac cac ccc tca 153  
 Leu Gly Thr Lys Thr Glu Ser Ser Ser Arg Gly Pro Tyr His Pro Ser  
 20 25 30

gag tgc tgc ttc acc tac act acc tac aag atc ccg cgt cag cgg att 201  
 Glu Cys Cys Phe Thr Tyr Thr Thr Tyr Lys Ile Pro Arg Gln Arg Ile  
 35 40 45

atg gat tac tat gag acc aac agc cag tgc tcc aag ccc gga att gtc 249  
 Met Asp Tyr Tyr Glu Thr Asn Ser Gln Cys Ser Lys Pro Gly Ile Val  
 50 55 60 65



ttc atc acc aaa agg ggc cat tcc gtc tgt acc aac ccc agt gac aag	297
Phe Ile Thr Lys Arg Gly His Ser Val Cys Thr Asn Pro Ser Asp Lys	
70 75 80	

tgg gtc cag gac tat atc aag gac atg aag gag aac tgagtgaccc	343
Trp Val Gln Asp Tyr Ile Lys Asp Met Lys Glu Asn	
85 90	

agaaggggtg gcgaaggcac agctcagaga cataaagaga agatgccaaag gccccctcct	403
ccaccacccc ctaactctca gccccagtca ccctcttgga gcttccctgc tttgaattaa	463
agaccactca tgctcttc	481

<210> 36  
 <211> 3709  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (885) ... (960)

<220>  
 <221> CDS  
 <222> (2149) ... (2260)

<220>  
 <221> CDS  
 <222> (3383) ... (3482)

<400> 36	
tctagaaaaa aaaaaacaaa aagggaaaat tcccctggca ggactctcag atgctgctga	60
gtagctctca gtcctctctg taacccaaac ataacacatc tatctccgtg cttacactgg	120
gtggctttca cttgtttatc tgtgaattga agagaagtg cttgaggta ggcagtgtc	180
ctcattggta actgccttct ctggggctaa ccaaggacct agaacagaat aagctattga	240
aaattgttga ggattgaaaa aaatagaaaa aatagaaatg gcaaatatct aggccagtca	300
ctggacatag agaattgtat ttaattctta tcgcacgtcc ttgagacatg tattgctatt	360
tgcattttgt gtgaatatgc atttgggtaa gtttatgtaa tccctcctct gcagaactgg	420
gattcaaatg caggtgtatc tctgttcagg tccagactct tctgcctga agcagtagta	480
cttggatgga atgacgtagg gttggacaag ccacacagag gccacttcct ctcacttact	540
tttctttgct tcccactcaa ccaggacagt tcccacgcac tttttcaaga ttcttatctg	600
ctccacact tggggaagtt cccaatgcaa cctatcaatc catcaccacc acgaatacca	660
gccaggagag gtggggaaag gagtttacca catggctcgt ggggtgtgagc aactgttccc	720
tgtccctatg gcttcccact tgtggctccc accatggcct ggagttttgg gtggagtttt	780
tcaaataaaa gccctcagca ttgcaggacg gcacagtggg gagctcttag cttcaccagg	840
ctcatcaaaag ctgctccagg aaggcccaag ccagaccaga agac atg cag atc atc	896
	Met Gln Ile Ile
	1

acc aca gcc ctg gtg tgc ttg ctg cta gct ggg atg tgg ccg gaa gat	944
Thr Thr Ala Leu Val Cys Leu Leu Leu Ala Gly Met Trp Pro Glu Asp	
5 10 15 20	

gtg gac agc aag agc a gtgagtgtgg caggcatcat tttgcttctc tctggggagg	1000
Val Asp Ser Lys Ser	
25	

gcagaaacgt ggtcagccac tctgggggttg gagcaggcct ctccttgaac tcaccaactc	1060
tatctcccct cttcctacct aaagaggagg aatgggtgaac ttggacaggc tgggggtgagg	1120
gctagtagga gaacatgag ttgggggcaa cacagagaac tgaactgaca gcttcagtac	1180
aaggagctct gcttcatcca gacccaagga agggaacctg tgagggtact cgggtaaagc	1240
tgggaggccc aaggtccagg ggacagcctg ggtgtagctt ctacagtgtg acagacacca	1300
agtagagtca gaaggcaaga ccgggctcta acaattggtc actcctgggc aagtcacttt	1360

agctctcaaa	ctctactttc	tctatcagtg	aaatggagtt	gatgatgtct	gccctccaag	1420									
actgttttga	gaataccaac	ctagtaagag	gcatgaaagg	gggtgcaaac	agaaaaacta	1480									
ggaggaagaa	gctgggattg	gaatgcaggt	ctcttgccgg	atgtggtgtg	ggaggagaat	1540									
gcacaaatgg	acagagtggg	ggttgggggc	tgggaaagag	ctaaggacca	gggcaggagg	1600									
ggattcaaga	gactgagtag	ggcagctagc	tagttcctgg	gagctcttcc	cttgtcatct	1660									
catcagtttg	gactcctcga	acaattccta	atcttcccca	gatcaggtct	gtgaactgtg	1720									
gaccactgtg	tcttgcacga	gactaaccag	gtccccaggg	tgtgggggtcc	agagcccttg	1780									
gacatgaata	ctggggcaga	accatgcaca	tgtggtgaaa	tacaaaaact	ggatgagcct	1840									
ttagaaacca	ggctccaaaa	agttttatct	tacagatggg	aagtctgggg	ccagggtgaa	1900									
ggcacatctt	cctcagggcc	actcagctgg	gggtgccccg	gctcagatct	gaaccccaat	1960									
cttctgactc	tttacctagc	cccagaacaa	gggtggtgat	gaggcagagc	tatgccggca	2020									
ccgtctggat	gtggtcccca	agccagggtc	tgtcctggga	ggcggttttt	tgtttgtttt	2080									
ttaaaaattg	tgctacaggt	gagaggttga	gaaatggatg	caaaccatcg	tctgtgttcc	2140									
tcttctag	tg	cag	gta	ccc	ttc	tcc	aga	tgt	tcg	ttc	tca	ttt	gcg	gag	2189
Met Gln Val Pro Phe Ser Arg Cys Cys Phe Ser Phe Ala Glu															
30 35															

caa	gag	att	ccc	ctg	agg	gca	atc	ctg	tgt	tac	aga	aat	acc	agc	tcc	2237
Gln	Glu	Ile	Pro	Leu	Arg	Ala	Ile	Leu	Cys	Tyr	Arg	Asn	Thr	Ser	Ser	
40 45 50 55																

atc	tgc	tcc	aat	gag	ggc	tta	at	gtaagtgatc	acctgctcaa	tctctcccta	2290
Ile	Cys	Ser	Asn	Glu	Gly	Leu	Ile				
60											

gagaacagaa	ccccgccagc	ctggaattac	aagagtagac	actagatgac	agtattttac	2350									
tgggaataagg	tttctaacc	cagagctgcc	agcacctggg	tgcaagccac	acttgggcgc	2410									
tagagggagc	gctgagcttc	ctagcaggtg	tgaggaagga	tgcacatgtg	ctcctgcagt	2470									
ggcttgtgtt	tcttgaact	ccaaggtgcc	aagtattgta	tcccagcatt	atgagctcag	2530									
aggtttaaca	aaagcatgag	gggttattgt	gcactggaaa	gagcaaggga	accagatgag	2590									
gttcttgcgc	ctggatttgg	aaccatagct	cttgggtgac	cgtggacagg	taactccttt	2650									
gtactgaatt	gtctgtgtat	ccttctgtat	tccttatctg	tgaagggtca	taaacatagc	2710									
tgcacacag	ggctctttaca	aacttaattg	gagtagcttt	cacataccag	tcagtatttt	2770									
aaggcttttt	catgtatatt	ctctctgtcg	atcctcttgg	ggcacatatt	tttgttatca	2830									
tgaagagtga	ggttcaggaa	ggtagagata	tttgtctaag	atcaaccaga	tagtaagaga	2890									
tagagttggg	ctatagattg	gacaatagtc	cagtttagga	agtagacaga	tcagaagaga	2950									
aaaatacaca	cccacacaca	cacacaaggc	gcgcgcacac	acacacacac	aaacacatga	3010									
gtccaacgca	acaagtaagg	cccagatggg	acacagaaac	attaaagttg	gtgcaaagag	3070									
ctattccagg	atgggaattt	ctcatctcac	ctaactgtca	gaatgttttc	agctgttcag	3130									
ccccaccctg	atacaccaaa	ttgaaaccag	gagaggggtc	caggaaattc	aattcataag	3190									
ctcctgggtg	tttggctgtt	ccccagcgtg	caaaccacac	atcctgtgca	gcaacttcat	3250									
ttacagaggg	gagcccaagg	cctagcaaga	gcagtttagg	ggacctggca	gccggaggag	3310									
gcggggcttg	tgctgtgccc	accagtggtg	ggcttgggtg	gctcagcctt	ctctcttatt	3370									
ctctgttcac	ag	a	ttc	aag	ctg	aag	aga	ggc	aaa	gag	gcc	tgc	gcc	ttg	3419
Phe Lys Leu Lys Arg Gly Lys Glu Ala Cys Ala Leu															
65 70 75															

gac	aca	gtt	gga	tgg	gtt	cag	agg	cac	aga	aaa	atg	ctg	agg	cac	tgc	3467
Asp	Thr	Val	Gly	Trp	Val	Gln	Arg	His	Arg	Lys	Met	Leu	Arg	His	Cys	
80 85 90																

ccg	tca	aaa	aga	aaa	tgagcagatt	tctttccatt	gtgggctctg	gaaaccacat	3522
Pro	Ser	Lys	Arg	Lys					
95									

ggcttcacct	gtccccgaaa	ctaccagccc	tacaccattc	cttctgccct	gcttttgcta	3582
ggtcacagag	gatctgcttg	gtcttgataa	gctatgttgt	tgcaacttta	acattttaaat	3642
tatacaatca	tcaaccccca	accctctggg	ctcttggatt	tcagagtga	aacttgatgg	3702
cattgag						3709

<210> 37  
 <211> 673  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (67)...(450)

<400> 37  
 gggcaactca ccctcactca gaggtcttct ggttctggaa acaactctag ctcagccttc 60  
 tccacc atg agc ctc aga ctt gat acc acc cct tcc tgt aac agt gcg 108  
 Met Ser Leu Arg Leu Asp Thr Thr Pro Ser Cys Asn Ser Ala  
 1 5 10  
 aga cca ctt cat gcc ttg cag gtg ctg ctg ctt ctg tca ttg ctg ctg 156  
 Arg Pro Leu His Ala Leu Gln Val Leu Leu Leu Leu Ser Leu Leu Leu  
 15 20 25 30  
 act gct ctg gct tcc tcc acc aaa gga caa act aag aga aac ttg gcg 204  
 Thr Ala Leu Ala Ser Ser Thr Lys Gly Gln Thr Lys Arg Asn Leu Ala  
 35 40 45  
 aaa ggc aaa gag gaa agt cta gac agt gac ttg tat gct gaa ctc cgc 252  
 Lys Gly Lys Glu Glu Ser Leu Asp Ser Asp Leu Tyr Ala Glu Leu Arg  
 50 55 60  
 tgc atg tgt ata aag aca acc tct gga att cat ccc aaa aac atc caa 300  
 Cys Met Cys Ile Lys Thr Thr Ser Gly Ile His Pro Lys Asn Ile Gln  
 65 70 75  
 agt ttg gaa gtg atc ggg aaa gga acc cat tgc aac caa gtc gaa gtg 348  
 Ser Leu Glu Val Ile Gly Lys Gly Thr His Cys Asn Gln Val Glu Val  
 80 85 90  
 ata gcc aca ctg aag gat ggg agg aaa atc tgc ctg gac cca gat gct 396  
 Ile Ala Thr Leu Lys Asp Gly Arg Lys Ile Cys Leu Asp Pro Asp Ala  
 95 100 105 110  
 ccc aga atc aag aaa att gta cag aaa aaa ttg gca ggt gat gaa tct 444  
 Pro Arg Ile Lys Lys Ile Val Gln Lys Lys Leu Ala Gly Asp Glu Ser  
 115 120 125  
 gct gat taatttgctt tggttctgcc aaacttcttt aactcccagg aagggtagaa 500  
 Ala Asp  
 ttttgaacc ttgattttct agagttctca tttattcagg atacctattc ttactgtatt 560  
 aaaatttgga tatgtgtttc attctgtctc aaaaatcaca ttttattctg agaaggttgg 620  
 ttaaaagatg gcagaaagaa gatgaaaata aataagcctg gtttcaaccc tct 673

<210> 38  
 <211> 12  
 <212> PRT  
 <213> Homo sapiens

<400> 38  
 Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln  
 1 5 10

<210> 39  
 <211> 2545  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (40)...(414)

```

<400> 39
atccaatata ggagtgactt ggaactccat tctatcact atg aag aaa agt ggt      54
                               Met Lys Lys Ser Gly
                               1           5

ggt ctt ttc ctc ttg ggc atc atc ttg ctg gtt ctg att gga gtg caa      102
Val Leu Phe Leu Leu Gly Ile Ile Leu Leu Val Leu Ile Gly Val Gln
                               10           15           20

gga acc cca gta gtg aga aag ggt cgc tgt tcc tgc atc agc acc aac      150
Gly Thr Pro Val Val Arg Lys Gly Arg Cys Ser Cys Ile Ser Thr Asn
                               25           30           35

caa ggg act atc cac cta caa tcc ttg aaa gac ctt aaa caa ttt gcc      198
Gln Gly Thr Ile His Leu Gln Ser Leu Lys Asp Leu Lys Gln Phe Ala
                               40           45           50

cca agc cct tcc tgc gag aaa att gaa atc att gct aca ctg aag aat      246
Pro Ser Pro Ser Cys Glu Lys Ile Glu Ile Ile Ala Thr Leu Lys Asn
                               55           60           65

gga gtt caa aca tgt cta aac cca gat tca gca gat gtg aag gaa ctg      294
Gly Val Gln Thr Cys Leu Asn Pro Asp Ser Ala Asp Val Lys Glu Leu
                               70           75           80           85

att aaa aag tgg gag aaa cag gtc agc caa aag aaa aag caa aag aat      342
Ile Lys Lys Trp Glu Lys Gln Val Ser Gln Lys Lys Lys Gln Lys Asn
                               90           95           100

ggg aaa aaa cat caa aaa aag aaa gtt ctg aaa gtt cga aaa tct caa      390
Gly Lys Lys His Gln Lys Lys Lys Val Leu Lys Val Arg Lys Ser Gln
                               105           110           115

cgt tct cgt caa aag aag act aca taagagacca cttaccaat aagtattctg      444
Arg Ser Arg Gln Lys Lys Thr Thr
                               120           125

tgtaaaaaat gttctatttt aattataccg ctatcattcc aaaggaggat ggcatataat      504
acaaaggctt attaatttga ctagaaaatt taaaacatta ctctgaaatt gtaactaaag      564
ttagaaagt gattttaaga atccaaacgt taagaattgt taaaggctat gattgtcttt      624
gttcttctac caccaccag ttgaatttca tcatgcttaa ggccatgatt ttagcaatac      684
ccatgtctac acagatgttc acccaaccac atcccactca caacagctgc ctggaagagc      744
agccctaggc ttccacgtac tgcagcctcc agagagtatc tgaggcacat gtcagcaagt      804
cctaagcctg ttagcatgct ggtgagccaa gcagtttgaa attgagctgg acctaccaa      864
gctgctgtgg ccatcaacct ctgtatttga atcagcctac aggcctcaca cacaatgtgt      924
ctgagagatt catgctgatt gttattgggt atcaccactg gagatcacca gtgtgtggct      984
ttcagagcct cctttctggc tttggaagcc atgtgattcc atcttgcccc ctcaggctga      1044
ccactttatt tctttttgtt cccctttgct tcattcaagt cagctcttct ccatectacc      1104
acaatgcagt gcctttcttc tctccagtgc acctgtcata tgctctgatt tatctgagtc      1164
aactcctttc tcatcttgtc cccaacaccc cacagaagtg ctttcttctc ccaattcatc      1224
ctcactcagt ccagcttagt tcaagtcctg cctcttaaata aaaccttttt ggacacacaa      1284
attatcttaa aactcctggt tcacttggtt cagtaccaca tgggtgaaca ctcaatgggt      1344

```

aactaattct	tgggtgttta	tcctatctct	ccaaccagat	tgtcagctcc	ttgagggcaa	1404
gagccacagt	atatttccct	gtttcttcca	cagtgcctaa	taatactgtg	gaactagggt	1464
ttaataattt	tttaattgat	gttgttatgg	gcaggatggc	aaccagacca	ttgtctcaga	1524
gcagggtgctg	gctcttttcc	ggctactcca	tgttggttag	cctctggtaa	cctcttactt	1584
attatcttca	ggacactcac	tacagggacc	agggatgatg	caacatcctt	gtctttttat	1644
gacaggatgt	ttgctcagct	tctccaacaa	taagaagcac	gtggtaaaac	acttgcggtat	1704
attctggact	gtttttaaaa	aatatacagt	ttaccgaaaa	tcatataatc	ttacaatgaa	1764
aaggacttta	tagatcagcc	agtgaccaac	cttttcccaa	ccatacaaaa	attccttttc	1824
ccgaaggaaa	agggctttct	caataagcct	cagctttcta	agatctaaca	agatagccac	1884
cgagatcctt	atcgaaactc	attttaggca	aatatgagtt	ttattgtccg	tttacttgtt	1944
tcagagtttg	tattgtgatt	atcaattacc	acaccatctc	ccatgaagaa	agggaaacggt	2004
gaagtactaa	gcgctagagg	aagcagccaa	gtcggttagt	ggaagcatga	ttgggtgcca	2064
gttagcctct	gcaggatgtg	gaaacctcct	tccaggggag	gttcagtga	ttgtgtagga	2124
gaggttgtct	gtggccagaa	tttaaacccta	tactcacttt	cccaaattga	atcactgctc	2184
acactgctga	tgatttagag	tgctgtccgg	tggagatccc	acccgaacgt	cttatctaata	2244
catgaaactc	cctagtccct	tcatgtaact	tccctgaaaa	atctaagtgt	ttcataaatt	2304
tgagagtctg	tgaccacatt	accttgcatc	tcacaggtag	acagtatata	actaacaacc	2364
aaagactaca	tattgtcact	gacacacacg	ttataatcat	ttatcatata	tatacataca	2424
tgcatacact	ctcaaagcaa	ataatttttc	acttcaaaac	agtattgact	tgtatacctt	2484
gtaatttgaa	atattttctt	tgttaaaata	gaatggtatc	aataaataga	ccattaatca	2544
g						2545

<210> 40  
 <211> 12  
 <212> PRT  
 <213> Homo sapiens

<400> 40  
 Glu Leu Cys Leu Asp Pro Lys Glu Asn Trp Val Gln  
 1 5 10

<210> 41  
 <211> 12  
 <212> PRT  
 <213> Homo sapiens

<400> 41  
 Glu Ile Cys Leu Asp Pro Glu Ala Pro Phe Leu Lys  
 1 5 10

<210> 42  
 <211> 12  
 <212> PRT  
 <213> Homo sapiens

<400> 42  
 Gln Val Cys Ala Asp Pro Ser Glu Glu Trp Val Gln  
 1 5 10

<210> 43  
 <211> 12  
 <212> PRT  
 <213> Homo sapiens

<400> 43  
 Gln Val Cys Ala Asp Pro Ser Glu Ser Trp Val Gln  
 1 5 10

<210> 44  
 <211> 12  
 <212> PRT  
 <213> Homo sapiens

<400> 44  
 Gln Val Cys Ala Asp Pro Ser Glu Ser Trp Val Gln  
 1 5 10

<210> 45  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 45  
 Met Lys Lys Ser Gly Val Leu Phe Leu Leu Gly Ile Ile Leu Leu Val  
 1 5 10 15  
 Leu Ile Gly Val Gln Gly Thr Pro Val Val Arg Lys Gly Arg Cys Ser  
 20 25 30  
 Cys Ile Ser Thr Asn Gln Gly Thr Ile His Leu Gln Ser Leu Lys Asp  
 35 40 45  
 Leu Lys Gln Phe Ala Pro Ser Pro Ser Cys Glu Lys Ile Glu Ile Ile  
 50 55 60  
 Ala Thr Leu Lys Asn Gly Val Gln Thr Cys Leu Asn Pro Asp Ser Ala  
 65 70 75 80  
 Asp Val Lys Glu Leu Ile Lys Lys Trp Glu Lys Gln Val Ser Gln Lys  
 85 90 95  
 Lys Lys Gln Lys Asn Gly Lys Lys His Gln Lys Lys Lys Val Leu Lys  
 100 105 110  
 Val Arg Lys Ser Gln Arg Ser Arg Gln Lys Lys Thr Thr  
 115 120 125

<210> 46  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens

<400> 46  
 Met Ser Leu Arg Leu Asp Thr Thr Pro Ser Cys Asn Ser Ala Arg Pro  
 1 5 10 15  
 Leu His Ala Leu Gln Val Leu Leu Leu Leu Ser Leu Leu Leu Thr Ala  
 20 25 30  
 Leu Ala Ser Ser Thr Lys Gly Gln Thr Lys Arg Asn Leu Ala Lys Gly  
 35 40 45  
 Lys Glu Glu Ser Leu Asp Ser Asp Leu Tyr Ala Glu Leu Arg Cys Met  
 50 55 60  
 Cys Ile Lys Thr Thr Ser Gly Ile His Pro Lys Asn Ile Gln Ser Leu  
 65 70 75 80  
 Glu Val Ile Gly Lys Gly Thr His Cys Asn Gln Val Glu Val Ile Ala  
 85 90 95  
 Thr Leu Lys Asp Gly Arg Lys Ile Cys Leu Asp Pro Asp Ala Pro Arg  
 100 105 110  
 Ile Lys Lys Ile Val Gln Lys Lys Leu Ala Gly Asp Glu Ser Ala Asp  
 115 120 125

<210> 47  
 <211> 96  
 <212> PRT  
 <213> Homo sapiens

<400> 47

Met	Gln	Ile	Ile	Thr	Ala	Leu	Val	Cys	Leu	Leu	Leu	Ala	Gly	Met	
1				5				10					15		
Trp	Pro	Glu	Asp	Val	Asp	Ser	Lys	Ser	Met	Gln	Val	Pro	Phe	Ser	Arg
			20					25					30		
Cys	Cys	Phe	Ser	Phe	Ala	Glu	Gln	Glu	Ile	Pro	Leu	Arg	Ala	Ile	Leu
		35					40					45			
Cys	Tyr	Arg	Asn	Thr	Ser	Ser	Ile	Cys	Ser	Asn	Glu	Gly	Leu	Ile	Phe
	50				55					60					
Lys	Leu	Lys	Arg	Gly	Lys	Glu	Ala	Cys	Ala	Leu	Asp	Thr	Val	Gly	Trp
65					70					75					80
Val	Gln	Arg	His	Arg	Lys	Met	Leu	Arg	His	Cys	Pro	Ser	Lys	Arg	Lys
			85						90					95	

<210> 48

<211> 93

<212> PRT

<213> Homo sapiens

<400> 48

Met	Lys	Ile	Ser	Val	Ala	Ala	Ile	Pro	Phe	Phe	Leu	Leu	Ile	Thr	Ile
1				5					10					15	
Ala	Leu	Gly	Thr	Lys	Thr	Glu	Ser	Ser	Ser	Arg	Gly	Pro	Tyr	His	Pro
			20					25					30		
Ser	Glu	Cys	Cys	Phe	Thr	Tyr	Thr	Thr	Tyr	Lys	Ile	Pro	Arg	Gln	Arg
		35					40					45			
Ile	Met	Asp	Tyr	Tyr	Glu	Thr	Asn	Ser	Gln	Cys	Ser	Lys	Pro	Gly	Ile
	50					55					60				
Val	Phe	Ile	Thr	Lys	Arg	Gly	His	Ser	Val	Cys	Thr	Asn	Pro	Ser	Asp
65					70					75					80
Lys	Trp	Val	Gln	Asp	Tyr	Ile	Lys	Asp	Met	Lys	Glu	Asn			
			85						90						

<210> 49

<211> 93

<212> PRT

<213> Homo sapiens

<400> 49

Met	Gln	Val	Ser	Thr	Ala	Ala	Leu	Ala	Val	Leu	Leu	Cys	Thr	Met	Ala
1				5					10					15	
Leu	Cys	Asn	Gln	Val	Leu	Ser	Ala	Pro	Leu	Ala	Ala	Asp	Thr	Pro	Thr
		20						25					30		
Ala	Cys	Cys	Phe	Ser	Tyr	Thr	Ser	Arg	Gln	Ile	Pro	Gln	Asn	Phe	Ile
		35					40					45			
Ala	Asp	Tyr	Phe	Glu	Thr	Ser	Ser	Gln	Cys	Ser	Lys	Pro	Ser	Val	Ile
	50					55					60				
Phe	Leu	Thr	Lys	Arg	Gly	Arg	Gln	Val	Cys	Ala	Asp	Pro	Ser	Glu	Glu
65					70					75					80
Trp	Val	Gln	Lys	Tyr	Val	Ser	Asp	Leu	Glu	Leu	Ser	Ala			
			85						90						

<210> 50

<211> 98

<212> PRT

<213> Homo sapiens

<400> 50  
Met Lys Val Ser Ala Val Leu Leu Cys Leu Leu Leu Met Thr Ala Ala  
1 5 10 15  
Phe Asn Pro Gln Gly Leu Ala Gln Pro Asp Ala Leu Asn Val Pro Ser  
20 25 30  
Thr Cys Cys Phe Thr Phe Ser Ser Lys Lys Ile Ser Leu Gln Arg Leu  
35 40 45  
Lys Ser Tyr Val Ile Thr Thr Ser Arg Cys Pro Gln Lys Ala Val Ile  
50 55 60  
Phe Arg Thr Lys Leu Gly Lys Glu Ile Cys Ala Asp Pro Lys Glu Lys  
65 70 75 80  
Trp Val Gln Asn Tyr Met Lys His Leu Gly Arg Lys Ala His Thr Leu  
85 90 95  
Lys Thr

<210> 51  
<211> 839  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (54) ... (344)

<400> 51  
caaccagaa accaccacct ctcacgccaa agctcacacc ttcagcctcc aac atg 56  
Met  
1  
aag gtc tcc gca gca ctt ctg tgg ctg ctg ctc ata gca gct gcc ttc 104  
Lys Val Ser Ala Ala Leu Leu Trp Leu Leu Leu Ile Ala Ala Ala Phe  
5 10 15  
agc ccc cag ggg ctc gct ggg cca gct tct gtc cca acc acc tgc tgc 152  
Ser Pro Gln Gly Leu Ala Gly Pro Ala Ser Val Pro Thr Thr Cys Cys  
20 25 30  
ttt aac ctg gcc aat agg aag ata ccc ctt cag cga cta gag agc tac 200  
Phe Asn Leu Ala Asn Arg Lys Ile Pro Leu Gln Arg Leu Glu Ser Tyr  
35 40 45  
agg aga atc acc agt ggc aaa tgt ccc cag aaa gct gtg atc ttc aag 248  
Arg Arg Ile Thr Ser Gly Lys Cys Pro Gln Lys Ala Val Ile Phe Lys  
50 55 60 65  
acc aaa ctg gcc aag gat atc tgt gcc gac ccc aag aag aag tgg gtg 296  
Thr Lys Leu Ala Lys Asp Ile Cys Ala Asp Pro Lys Lys Lys Trp Val  
70 75 80  
cag gat tcc atg aag tat ctg gac caa aaa tct cca act cca aag cca 344  
Gln Asp Ser Met Lys Tyr Leu Asp Gln Lys Ser Pro Thr Pro Lys Pro  
85 90 95  
taaataatca ccatttttga aaccaaacca gagcctgagt gttgcctaata ttgttttccc 404  
ttcttacaat gcattctgag gtaacctcat tatcagtgca aagggcatgg gttttattat 464  
atatatatat atatattttt ttttaaaaaa aaacgtattg catttaattt attgaggctt 524  
taaaacttat cctccatgaa tatcagttat ttttaaaactg taaagctttg tgcagattct 584  
ttacccccctg ggagcccaaa ttcgatcccc tgtcacgtgt gggcaatgtt cccctctcc 644  
tctcttcctc cctggaatct tgtaaaaggc ctggcaaaaga tgatcagtat gaaaatgtca 704  
ttgttcttgt gaacccaaag tgtgactcat taaatggaag taatgttggt ttaggaatac 764



ataaagtatg tgcataaaaa attatagtca ctagttgtaa tttttttgtg ggaaatccac  
actgagctga ggggg

824  
839

<210> 52  
<211> 114  
<212> PRT  
<213> Homo sapiens

<400> 52  
Met Ser Leu Leu Ser Ser Arg Ala Ala Arg Val Pro Gly Pro Ser Ser  
1 5 10 15  
Ser Leu Cys Ala Leu Leu Val Leu Leu Leu Leu Thr Gln Pro Gly  
20 25 30  
Pro Ile Ala Ser Ala Gly Pro Ala Ala Ala Val Leu Arg Glu Leu Arg  
35 40 45  
Cys Val Cys Leu Gln Thr Thr Gln Gly Val His Pro Lys Met Ile Ser  
50 55 60  
Asn Leu Gln Val Phe Ala Ile Gly Pro Gln Cys Ser Lys Val Glu Val  
65 70 75 80  
Val Ala Ser Leu Lys Asn Gly Lys Glu Ile Cys Leu Asp Pro Glu Ala  
85 90 95  
Pro Phe Leu Lys Lys Val Ile Gln Lys Ile Leu Asp Gly Gly Asn Lys  
100 105 110  
Glu Asn

<210> 53  
<211> 107  
<212> PRT  
<213> Homo sapiens

<400> 53  
Met Ala Arg Ala Thr Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu  
1 5 10 15  
Arg Val Ala Leu Leu Leu Leu Val Ala Ala Ser Arg Arg Ala  
20 25 30  
Ala Gly Ala Pro Leu Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr  
35 40 45  
Leu Gln Gly Ile His Leu Lys Asn Ile Gln Ser Val Lys Val Lys Ser  
50 55 60  
Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn  
65 70 75 80  
Gly Gln Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Lys Lys Ile  
85 90 95  
Ile Glu Lys Met Leu Lys Asn Gly Lys Ser Asn  
100 105

<210> 54  
<211> 98  
<212> PRT  
<213> Homo sapiens

<400> 54  
Met Asn Pro Ser Ala Ala Val Ile Phe Cys Leu Ile Leu Leu Gly Leu  
1 5 10 15  
Ser Gly Thr Gln Gly Ile Pro Leu Ala Arg Thr Val Arg Cys Asn Cys  
20 25 30  
Ile His Ile Asp Asp Gly Pro Val Arg Met Arg Ala Ile Gly Lys Leu  
35 40 45

Glu Ile Ile Pro Ala Ser Leu Ser Cys Pro Arg Val Glu Ile Ile Ala  
 50 55 60  
 Thr Met Lys Lys Asn Asp Glu Gln Arg Cys Leu Asn Pro Glu Ser Lys  
 65 70 75 80  
 Thr Ile Lys Asn Leu Met Lys Ala Phe Ser Gln Lys Arg Ser Lys Arg  
 85 90 95  
 Ala Pro

<210> 55  
 <211> 1041  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (18) ... (338)

<400> 55  
 cccgcctgct gagcccc atg gcc cgc gct gct ctc tcc gcc gcc ccc agc 50  
 Met Ala Arg Ala Ala Leu Ser Ala Ala Pro Ser  
 1 5 10  
 aat ccc cgg ctc ctg cga gtg gca ctg ctg ctc ctg ctc ctg gta gcc 98  
 Asn Pro Arg Leu Leu Arg Val Ala Leu Leu Leu Leu Leu Val Ala  
 15 20 25  
 gct ggc cgg cgc gca gca gga gcg tcc gtg gcc act gaa ctg cgc tgc 146  
 Ala Gly Arg Arg Ala Ala Gly Ala Ser Val Ala Thr Glu Leu Arg Cys  
 30 35 40  
 cag tgc ttg cag acc ctg cag gga att cac ccc aag aac atc caa agt 194  
 Gln Cys Leu Gln Thr Leu Gln Gly Ile His Pro Lys Asn Ile Gln Ser  
 45 50 55  
 gtg aac gtg aag tcc ccc gga ccc cac tgc gcc caa acc gaa gtc ata 242  
 Val Asn Val Lys Ser Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile  
 60 65 70 75  
 gcc aca ctc aag aat ggg cgg aaa gct tgc ctc aat cct gca tcc ccc 290  
 Ala Thr Leu Lys Asn Gly Arg Lys Ala Cys Leu Asn Pro Ala Ser Pro  
 80 85 90  
 ata gtt aag aaa atc atc gaa aag atg ctg aac agt gac aaa tcc aac 338  
 Ile Val Lys Lys Ile Ile Glu Lys Met Leu Asn Ser Asp Lys Ser Asn  
 95 100 105  
 tgaccagaag ggaggaggaa gctcactggt ggctgttcct gaaggaggcc ctgcccttat 398  
 aggaacagaa gaggaaagag agacacagct gcagaggcca cctggattgt gcctaattgtg 458  
 tttgagcatc gcttaggaga agtcttctat ttatttattt attcattagt tttgaagatt 518  
 ctatgttaat atttttaggtg taaaataatt aagggtatga ttaactctac ctgcacactg 578  
 tcctattata ttcattcttt ttgaaatgtc aacccaagt tagttcaatc tggattcata 638  
 tttaatttga aggtagaatg ttttcaaatg ttctccagtc attatgttaa tatttctgag 698  
 gagcctgcaa catgccagcc actgtgatag aggctggcgg atccaagcaa atggccaatg 758  
 agatcattgt gaaggcaggg gaatgtatgt gcacatctgt tttgtaactg tttagatgaa 818  
 tgtcagttgt tatttattga aatgatttca cagtgtgtgg tcaacatttc tcatgttgaa 878  
 actttaagaa ctaaaatggt ctaaatatcc cttggacatt ttatgtcttt cttgtaaggc 938  
 atactgcctt gtttaatggt agttttacag tgtttctggc ttagaacaaa ggggcttaat 998  
 tattgatggt ttcatagaga atataaaaaat aaagcactta tag 1041

<210> 56  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 56  
 Met Asn Ala Lys Val Val Val Val Leu Val Leu Val Leu Thr Ala Leu  
 1 5 10 15  
 Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys  
 20 25 30  
 Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys  
 35 40 45  
 Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys  
 50 55 60  
 Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln  
 65 70 75 80  
 Glu Tyr Leu Glu Lys Ala Leu Asn Lys Arg Phe Lys Met  
 85 90

<210> 57  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens

<400> 57  
 Met Ala Arg Ala Ala Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu  
 1 5 10 15  
 Arg Val Ala Leu Leu Leu Leu Leu Val Ala Ala Gly Arg Arg Ala  
 20 25 30  
 Ala Gly Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr  
 35 40 45  
 Leu Gln Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val Lys Ser  
 50 55 60  
 Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn  
 65 70 75 80  
 Gly Arg Lys Ala Cys Leu Asn Pro Ala Ser Pro Ile Val Lys Lys Ile  
 85 90 95  
 Ile Glu Lys Met Leu Asn Ser Asp Lys Ser Asn  
 100 105

<210> 58  
 <211> 1560  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (102)...(398)

<400> 58  
 ctccataagg cactaaacttt cagagacagc agagcacaca agcttctagg acaagagcca 60  
 ggaagaaacc accggaagga accatctcac tgtgtgtaaa c atg act tcc aag ctg 116  
 Met Thr Ser Lys Leu  
 1 5  
 gcc gtg gct ctc ttg gca gcc ttc ctg att tct gca gct ctg tgt gaa 164  
 Ala Val Ala Leu Leu Ala Ala Phe Leu Ile Ser Ala Ala Leu Cys Glu  
 10 15 20

ggt gca gtt ttg cca agg agt gct aaa gaa ctt aga tgt cag tgc ata 212  
 Gly Ala Val Leu Pro Arg Ser Ala Lys Glu Leu Arg Cys Gln Cys Ile  
                   25                                  30                                  35

aag aca tac tcc aaa cct ttc cac ccc aaa ttt atc aaa gaa ctg aga 260  
 Lys Thr Tyr Ser Lys Pro Phe His Pro Lys Phe Ile Lys Glu Leu Arg  
                   40                                  45                                  50

gtg att gag agt gga cca cac tgc gcc aac aca gaa att att gta aag 308  
 Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr Glu Ile Ile Val Lys  
                   55                                  60                                  65

ctt tct gat gga aga gag ctc tgt ctg gac ccc aag gaa aac tgg gtg 356  
 Leu Ser Asp Gly Arg Glu Leu Cys Leu Asp Pro Lys Glu Asn Trp Val  
                   70                                  75                                  80                                  85

cag agg gtt gtg gag aag ttt ttg aag agg gct gag aat tca 398  
 Gln Arg Val Val Glu Lys Phe Leu Lys Arg Ala Glu Asn Ser  
                                   90                                  95

taaaaaaatt cattctctgt ggtatccaag aatcagtgaa gatgccagtg aaacttcaag 458  
 caaatctact tcaacacttc atgtattgtg tgggtctggt gtaggggtgc cagatgcaat 518  
 acaagattcc tgggttaaatt tgaatttcag taaacaatga atagtttttc attgtaccat 578  
 gaaatatcca gaacatactt atatgtaaag tattattttat ttgaatctac aaaaaacaac 638  
 aaataatttt taaatataag gattttccta gatattgcac gggagaatat acaaatagca 698  
 aaattgggcc aagggcccaag agaatatccg aactttaatt tcaggaattg aatggggttg 758  
 ctagaatgtg atatttgaag catcacataa aaatgatggg acaataaatt ttgccataaa 818  
 gtcaaattta gctggaaatc ctggattttt ttctgttaaa tctggcaacc ctagtctgct 878  
 agccaggatc cacaaagtcct tgttccactg tgccttggtt tctcctttat ttctaagtgg 938  
 aaaaagtatt agccaccatc ttacctcaca gtgatgtgtg gaggacatgt ggaagcactt 998  
 taagtttttt catcataaca taaattattt tcaagtgtaa cttattaacc tattttattat 1058  
 ttatgtattt atttaagcat caaatatttg tgcaagaatt tggaaaaata gaagatgaat 1118  
 cattgattga atagttataa agatgttata gtaaatttat tttatttttag atattaaatg 1178  
 atgttttatt agataaattt caatcagggt ttttagatta aacaaacaaa caattgggta 1238  
 cccagttaaa ttttcatttc agatatacaa caaataattt tttagtataa gtacattatt 1298  
 gtttatctga aatttttaatt gaactaacia tcctagtgtg atactcccag tcttgtcatt 1358  
 gccagctgtg ttggtagtgc tgtgttgaat tacggaataa tgagttagaa ctattaaaac 1418  
 agccaaaact ccacagtcac tattagtaat ttcttgctgg ttgaaacttg tttattatgt 1478  
 acaaatagat tcttataata ttattttaat gactgcattt ttaaatataa ggctttatat 1538  
 ttttaacttt aaaaaaaaacc gg 1560

<210> 59  
 <211> 15  
 <212> PRT  
 <213> Homo sapiens

<400> 59  
 Asn Leu Gln Val Phe Ala Ile Gly Pro Gln Cys Ser Lys Val Glu  
   1                                  5                                  10                                  15

<210> 60  
 <211> 14  
 <212> PRT  
 <213> Homo sapiens

<400> 60  
 Val Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala  
   1                                  5                                  10

<210> 61  
<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 61  
Val Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val  
1 5 10 15

<210> 62  
<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 62  
Glu Ser Tyr Arg Arg Ile Thr Asn Ile Gln Cys Pro Lys Glu Ala  
1 5 10 15

<210> 63  
<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 63  
Glu Ser Tyr Arg Arg Thr Thr Ser Ser His Cys Pro Arg Glu Ala  
1 5 10 15

<210> 64  
<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 64  
Lys Ser Tyr Val Ile Thr Thr Ser Arg Cys Pro Gln Lys Ala Val  
1 5 10 15

<210> 65  
<211> 12  
<212> PRT  
<213> Homo sapiens

<400> 65  
Glu Ile Cys Ala Asp Pro Lys Glu Lys Trp Val Gln  
1 5 10

<210> 66  
<211> 12  
<212> PRT  
<213> Homo sapiens

<400> 66  
Glu Ile Cys Ala Asp Pro Thr Gln Lys Trp Val Gln  
1 5 10

<210> 67  
 <211> 12  
 <212> PRT  
 <213> Homo sapiens

<400> 67  
 Glu Ile Cys Ala Asp Pro Lys Glu Arg Trp Val Arg  
 1 5 10

<210> 68  
 <211> 12  
 <212> PRT  
 <213> Homo sapiens

<400> 68  
 Asp Ile Cys Ala Asp Pro Lys Lys Lys Trp Val Gln  
 1 5 10

<210> 69  
 <211> 15  
 <212> PRT  
 <213> Homo sapiens

<400> 69  
 Ser Val Asn Val Lys Ser Pro Gly Pro His Cys Ala Gln Thr Glu  
 1 5 10 15

<210> 70  
 <211> 15  
 <212> PRT  
 <213> Homo sapiens

<400> 70  
 Ser Val Lys Val Lys Ser Pro Gly Pro His Cys Ala Gln Thr Glu  
 1 5 10 15

<210> 71  
 <211> 15  
 <212> PRT  
 <213> Homo sapiens

<400> 71  
 Ser Val Asn Val Arg Ser Pro Gly Pro His Cys Ala Gln Thr Glu  
 1 5 10 15

<210> 72  
 <211> 12  
 <212> PRT  
 <213> Homo sapiens

<400> 72  
 Lys Ala Cys Leu Asn Pro Ala Ser Pro Ile Val Lys  
 1 5 10

<210> 73  
 <211> 12  
 <212> PRT  
 <213> Homo sapiens

<400> 73  
 Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Lys  
 1 5 10

<210> 74  
 <211> 12  
 <212> PRT  
 <213> Homo sapiens

<400> 74  
 Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Gln  
 1 5 10

<210> 75  
 <211> 12  
 <212> PRT  
 <213> Homo sapiens

<400> 75  
 Lys Ser Tyr Lys Ile Ile Thr Ser Ser Lys Cys Pro  
 1 5 10

<210> 76  
 <211> 661  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (32)...(331)

<400> 76  
 tcaaactgaa gctcgcactc tcgcctccag c atg aaa gtc tct gcc gcc ctt 52  
 Met Lys Val Ser Ala Ala Leu  
 1 5

ctg tgc ctg ctg ctc ata gca gcc acc ttc att ccc caa ggg ctc gct 100  
 Leu Cys Leu Leu Leu Ile Ala Ala Thr Phe Ile Pro Gln Gly Leu Ala  
 10 15 20

cag cca gat gca atc aat gcc cca gtc acc tgc tgc tat aac ttc acc 148  
 Gln Pro Asp Ala Ile Asn Ala Pro Val Thr Cys Cys Tyr Asn Phe Thr  
 25 30 35

aat agg aag atc tca gtg cag agg ctc gcg agc tat aga aga atc acc 196  
 Asn Arg Lys Ile Ser Val Gln Arg Leu Ala Ser Tyr Arg Arg Ile Thr  
 40 45 50 55

agc agc aag tgt ccc aaa gaa gct gtg atc ttc aag acc att gtg gcc 244  
 Ser Ser Lys Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Ile Val Ala  
 60 65 70

aag gag atc tgt gct gac ccc aag cag aag tgg gtt cag gat tcc atg 292  
 Lys Glu Ile Cys Ala Asp Pro Lys Gln Lys Trp Val Gln Asp Ser Met  
                   75                                  80                                  85

gac cac ctg gac aag caa acc caa act ccg aag act tga acactcactc 341  
 Asp His Leu Asp Lys Gln Thr Gln Thr Pro Lys Thr \*  
                   90                                  95

cacaacccaa gaatctgcag ctaacttatt ttcccctagc tttccccaga catcctgttt 401  
 tattttatta taatgaattt tgtttgttga tgtgaaacat tatgccttaa gtaatgttaa 461  
 ttcttattta agttattgat gttttaagtt tatctttcat ggtactagtg ttttttagat 521  
 acagagactt ggggaaattg cttttcctct tgaaccacag ttctaccctt gggatgtttt 581  
 gagggctctt gcaagaatca tttttttaac attccaatgc atttaataca aagaattgct 641  
 aaaatattat tgtggaaatg 661

<210> 77  
 <211> 1847  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (80) ... (346)

<400> 77  
 tctccgtcag ccgcattgcc cgctcggcgt ccggcccccg acccgtgctc gtccgcccgc 60  
 ccgccccgcc gcccgcgcc atg aac gcc aag gtc gtg gtc gtg ctg gtc ctc 112  
                                   Met Asn Ala Lys Val Val Val Val Leu Val Leu  
   1                                  5                                  10

gtg ctg acc gcg ctc tgc ctc agc gac ggg aag ccc gtc agc ctg agc 160  
 Val Leu Thr Ala Leu Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser  
                                   15                                  20                                  25

tac aga tgc cca tgc cga ttc ttc gaa agc cat gtt gcc aga gcc aac 208  
 Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn  
                                   30                                  35                                  40

gtc aag cat ctc aaa att ctc aac act cca aac tgt gcc ctt cag att 256  
 Val Lys His Leu Lys Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile  
                                   45                                  50                                  55

gta gcc cgg ctg aag aac aac aac aga caa gtg tgc att gac ccg aag 304  
 Val Ala Arg Leu Lys Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys  
                   60                                  65                                  70                                  75

cta aag tgg att cag gag tac ctg gag aaa gct tta aac aag 346  
 Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn Lys  
                                   80                                  85

taagcacaac agccaaaaag gactttccgc tagaccact cgaggaaaac taaaaccttg 406  
 tgagagatga aagggcaaaag acgtggggga gggggcctta accatgagga ccagggtgtgt 466  
 gtgtgggggtg ggcacattga tctgggatcg ggctgaggt ttgcagcatt tagaccctgc 526  
 atttatagca tacggtatga tattgcagct tatattcatc catgccctgt acctgtgcac 586  
 gttggaactt ttattactgg ggtttttcta agaaagaaat tgtattatca acagcatttt 646  
 caagcagtta gttccttcat gatcatcaca atcatcatca ttctcattct cattttttta 706  
 atcaacgagt acttcaagat ctgaatttgg cttgttttga gcatctcctc tgctcccttg 766  
 gggagtctgg gcacagtcag gtggtggctt aacaggggagc tggaaaaagt gtcctttctt 826  
 cagacactga ggctcccgca gcagcgcccc tcccaagagg aaggcctctg tggcactcag 886  
 ataccgactg gggctggggc gccgccactg ccttcacctc ctctttcaaa cctcagtgat 946  
 tggctctgtg ggctccatgt agaagccact attactggga ctgtctcaga gaccctctc 1006  
 ccagctattc ctactctctc cccgactccg agagcatgct taatcttgct tctgcttctc 1066



atttctgtag	cctgatcagc	gccgcaccag	ccgggaagag	ggtgattgct	ggggctcgtg	1126
ccctgcatcc	ctctcctccc	agggcctgcc	ccacagctcg	ggccctctgt	gagatccgtc	1186
tttggcctcc	tccagaatgg	agctggccct	ctcctgggga	tgtgtaatgg	ttccccctgct	1246
taccgcaaaa	agacaagtct	ttacagaatc	aaatgcaatt	ttaaatctga	gagctcgctt	1306
gagtgactgg	gtttgtgatt	gcctctgaag	cctatgtatg	ccatggaggc	actaacaac	1366
tctgaggttt	ccgaaatcag	aagcgaaaaa	atcagtgaat	aaaccatcat	cttgccacta	1426
ccccctcctg	aagccacagc	aggggttcag	gttccaatca	gaactgttgg	caaggtgaca	1486
tttccatgca	tagatgcat	ccacagaagg	tcctgggtgt	atttgtaact	ttttgcaagg	1546
cattttttta	tatatatttt	tgtgcacatt	tttttttacg	attcctttaga	aaacaaatgt	1606
atttcaaaat	atatttatag	tcgaacaagt	catatatatg	aatgagagcc	atatgaatgt	1666
cagtagttta	tacttctcta	ttatctcaaa	ctactggcaa	tttgtaaaga	aatatatatg	1726
atatataaat	gtgattgcag	cttttcaatg	ttagccacag	tgtatttttt	cacttgtact	1786
aaaattgtat	caaatgtgac	attatatgca	ctagcaataa	aatgctaatt	gtttcatggt	1846
a						1847

<210> 78  
 <211> 1160  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (27) ... (299)

<400> 78																
cctccgacag	cctctccaca	ggtacc	atg	aag	gtc	tcc	gcg	gca	cgc	ctc	gct					53
			Met	Lys	Val	Ser	Ala	Ala	Arg	Leu	Ala					
			1					5								
gtc	atc	ctc	att	gct	act	gcc	ctc	tgc	gct	cct	gca	tct	gcc	tcc	cca	101
Val	Ile	Leu	Ile	Ala	Thr	Ala	Leu	Cys	Ala	Pro	Ala	Ser	Ala	Ser	Pro	
10					15					20					25	
tat	tcc	tcg	gac	acc	aca	ccc	tgc	tgc	ttt	gcc	tac	att	gcc	cgc	cca	149
Tyr	Ser	Ser	Asp	Thr	Thr	Pro	Cys	Cys	Phe	Ala	Tyr	Ile	Ala	Arg	Pro	
				30					35					40		
ctg	ccc	cgt	gcc	cac	atc	aag	gag	tat	ttc	tac	acc	agt	ggc	aag	tgc	197
Leu	Pro	Arg	Ala	His	Ile	Lys	Glu	Tyr	Phe	Tyr	Thr	Ser	Gly	Lys	Cys	
			45					50					55			
tcc	aac	cca	gca	gtc	gtc	ttt	gtc	acc	cga	aag	aac	cgc	caa	gtg	tgt	245
Ser	Asn	Pro	Ala	Val	Val	Phe	Val	Thr	Arg	Lys	Asn	Arg	Gln	Val	Cys	
		60					65					70				
gcc	aac	cca	gag	aag	aaa	tgg	gtt	cgg	gag	tac	atc	aac	tct	ttg	gag	293
Ala	Asn	Pro	Glu	Lys	Lys	Trp	Val	Arg	Glu	Tyr	Ile	Asn	Ser	Leu	Glu	
	75					80					85					
atg	agc	taggatggag	agtccttgaa	cctgaactta	cacaaatttg	cctgtttctg										349
Met	Ser															
90																

cttgctcttg	tcctagcttg	ggaggcttcc	cctcactatc	ctacccccacc	cgctccttga	409
agggccca	ttctgaccac	gacgagcagc	agttacaaaa	accttcccca	ggctggacgt	469
ggtggctcag	ccttgtaatc	ccagcacttt	gggaggccaa	ggtgggtgga	tcacttgagg	529
tcaggagttc	gagacagcct	ggccaacatg	atgaaacccc	atgtgtacta	aaaatacaaa	589
aaattagccg	ggcgtggtag	cgggcgcctg	tagtcccagc	tactcggggag	gctgaggcgag	649
gagaatggcg	tgaacccggg	agcggagctt	gcagtgcgac	gagatcgcg	cactgcactc	709
cagcctgggc	gacagagcga	gactccgtct	caaaaaaaaaa	aaaaaaaaaa	aaaaaaatac	769
aaaaattagc	cgcgtgggtg	cccacgcctg	taatcccagc	tactcggggag	gctaaggcgag	829
gaaaattggt	tgaacccagg	aggtggaggc	tgcagtgcgc	tgagattgtg	ccacttcact	889

ccagcctggg	tgacaaagtg	agactccgtc	acaacaacaa	caacaaaaag	cttccccaac	949
taaagcctag	aagagcttct	gaggecgctgc	tttgtcaaaa	ggaagtctct	aggttctgag	1009
ctctggcttt	gccttggctt	tgcaagggct	ctgtgacaag	gaaggaagtc	agcatgcctc	1069
tagaggcaag	gaagggagga	acactgcact	cttaagcttc	cgccgtctca	acccttcaca	1129
ggagcttact	ggcaaacatg	aaaaatcggg	g			1160

<210> 79  
 <211> 696  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (109) ... (384)

<400> 79	
ttcccccccc	cccccccccc
ccccgcccga	gcacaggaca
cagctggggt	ctgaagcttc
60	
tgagttctgc	agcctcacct
ctgagaaaac	ctcttttcca
ccaatacc	atg aag ctc
117	
	Met Lys Leu
	1

tgc gtg act gtc ctg tct ctc ctc atg cta gta gct gcc ttc tgc tct	165
Cys Val Thr Val Leu Ser Leu Leu Met Leu Val Ala Ala Phe Cys Ser	
5 10 15	

cca gcg ctc tca gca cca atg ggc tca gac cct ccc acc gcc tgc tgc	213
Pro Ala Leu Ser Ala Pro Met Gly Ser Asp Pro Pro Thr Ala Cys Cys	
20 25 30 35	

ttt tct tac acc gcg agg aag ctt cct cgc aac ttt gtg gta gat tac	261
Phe Ser Tyr Thr Ala Arg Lys Leu Pro Arg Asn Phe Val Val Asp Tyr	
40 45 50	

tat gag acc agc agc ctc tgc tcc cag cca gct gtg gta ttc caa acc	309
Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val Phe Gln Thr	
55 60 65	

aaa aga agc aag caa gtc tgt gct gat ccc agt gaa tcc tgg gtc cag	357
Lys Arg Ser Lys Gln Val Cys Ala Asp Pro Ser Glu Ser Trp Val Gln	
70 75 80	

gag tac gtg tat gac ctg gaa ctg aac tgagctgctc agagacagga	404
Glu Tyr Val Tyr Asp Leu Glu Leu Asn	
85 90	

agtcttcagg	gaaggtcacc	tgagcccga	tgcttctcca	tgagacacat	ctcctccata	464
ctcaggactc	ctctccgcag	ttcctgtccc	ttctcttaat	ttaatctttt	ttatgtgccg	524
tgttattgta	ttaggtgtca	tttccattat	ttatattagt	ttagccaaag	gataagtgtc	584
ctatggggat	gggccactgt	cactgtttct	ctgctgttgc	aaatacatgg	ataacacatt	644
tgattctgtg	tgttttccat	aataaaaactt	taaaataaaa	tcgagacagt	ta	696

<210> 80  
 <211> 2738  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (123) ... (353)

<400> 80

gaacaaccca	gaaaccttca	cctctcatgc	tgaagctcac	acccttgccc	tccaagatga	60
aggtttctgc	agcgcttctg	tgectgctgc	tcatggcagc	cactttcagc	cctcagggac	120
tt gct cag	cca gat tca	gtt tcc att	cca atc acc	tgc tgc ttt	aac	167
Ala Gln	Pro Asp	Ser Val	Ser Ile	Pro Ile	Thr Cys Cys Phe Asn	
1	5		10		15	
gtg atc	aat agg	aaa att	cct atc	cag agg	ctg gag	215
Val Ile	Asn Arg	Lys Ile	Pro Ile	Gln Arg	Leu Glu	
	20		25		30	
atc acc	aac atc	caa tgt	ccc aag	gaa gct	gtg atc	263
Ile Thr	Asn Ile	Gln Cys	Pro Lys	Glu Ala	Val Ile	
	35		40		45	
cgg ggc	aag gag	gtc tgt	gct gac	ccc aag	gag aga	311
Arg Gly	Lys Glu	Val Cys	Ala Asp	Pro Lys	Glu Arg	
	50		55		60	
tcc atg	aag cat	ctg gac	caa ata	ttt caa	aat ctg	353
Ser Met	Lys His	Leu Asp	Gln Ile	Phe Gln	Asn Leu	
	65		70		75	
tgagccttca	tacatggact	gagagtcaga	gcttgaagaa	aagcttattt	attttcccca	413
acctcccca	ggtgcagtgt	gacattattt	tattataaca	tccacaaaga	gattattttt	473
aaataattta	aagcataata	tttcttaaaa	agtattttaat	tatattttaag	ttgttgatgt	533
tttaactcta	tctgtcatat	atcctagtga	atgtaaaatg	caaaatcctg	gtgatgtgtt	593
ttttgttttt	gttttcctgt	gagctcaact	aagttcacgg	caaaatgtca	ttgttctccc	653
tcctacctgt	ctgtagtgtt	gtggggctct	cccatggatc	atcaagggtga	aacactttgg	713
tattcttttg	caatcagtg	tctgttaagt	caaatgtgtg	ctttgtactg	ctgttggtga	773
aattgatgtt	actgtatata	actatggaat	tttgaaaaaa	aatttcaaaa	agaaaaaaat	833
atatataatt	taaaactaag	aaaaaaaaaa	aaaaaaaaaa	aaaaagggtt	ctattgactt	893
gggttaaatcg	tgtgaccg	gtggctggca	cgaaattgac	caaccctggg	gttagtatag	953
cttagttaaa	ctttcgttta	ttgctaaagg	ttaatcactg	ctgtttcccg	tgggggtgtg	1013
gctaggctaa	gcgttttgag	ctgcattgct	gcgtgcttga	tgcttgctcc	ttttgatcgt	1073
ggtgatattag	agggtgaact	cactggaatg	gggatgcttg	catgtgtaat	cttactaaga	1133
gctaatagaa	aggctaggac	caaaccagaa	acctccaatt	ctcatgtgga	agcccatgcc	1193
ctcaccctcc	aacatgaaag	cctctgcagc	acttctgtgt	ctgctgtctca	cagcagctgc	1253
tttcagcccc	caggggcttg	ctcagccagt	tgggattaat	acttcaacta	cctgtgtcta	1313
cagattttatc	aataagaaaa	ttccctaagca	gaggctggag	agctacagaa	ggaccaccag	1373
tagccactgt	ccccgggaag	ctgtaatctt	caagacccaa	ctggacaagg	agatctgtgc	1433
tgacccca	cagaagtggg	ttcaggactt	tatgaagcac	ctggacaaga	aaacccaaac	1493
tccaaagctt	tgaacattca	tgactgaact	gaaaacaagc	catgacttga	gaaacaaata	1553
atttgataac	cctgtccttt	ctcagagtgg	ttctgagatt	attttaaatct	aattctaagg	1613
aatatgagct	ttatgtaata	atgtgaatca	tggtttttct	tagtagattt	taaaagttat	1673
taatatttta	atttaattct	ccatggattt	tgggtgggtt	tgaacataaa	gccttggtatg	1733
tatatgtcat	ctcagtgtctg	taaaaactgt	gggatgctcc	tcccttctct	acctcatggg	1793
ggtattgtat	aagtccttgc	aagaatcagt	gcaaagattt	gctttaattg	ttaagatatg	1853
atgtccctat	ggaagcatat	tgttattata	taattacata	tttgcatatg	tatgactccc	1913
aaattttcac	ataaaataga	tttttgata	acaaaaaa	aaaaaaaaaa	aaggacacgg	1973
gcagcagaca	gtggtcagtc	ctttcttggc	tctgctgaca	ctcgagccca	cattccgtca	2033
cctgtctcaga	atcatgcagg	tctccactgc	tgcccttgct	gtcctcctct	gcaccatggc	2093
tctctgcaac	cagttctctg	catcacttgc	tgctgacacg	ccgaccgcct	gctgcttcag	2153
ctacacctcc	cggcagattc	cacagaattt	catagctgac	tactttgaga	cgagcagcca	2213
gtgctccaag	ccgggtgtca	tcttcttaac	caagcgaagc	cggcagggtct	gtgctgacct	2273
cagtgaggag	tgggtccaga	aatatgtcag	cgacctggag	ctgagtgcct	gaggggtcca	2333
gaagcttcga	ggccacgcga	cctcggtggg	cccagtgggg	aggagcagga	gcctgagcct	2393
tgggaacatg	cgtgtgacct	ccacagctac	ctcttctatg	gactggttgt	tgccaaacag	2453
ccacactgtg	ggactcttct	taacttaaat	tttaatttat	ttatactatt	tagtttttgt	2513
aatttatatt	cgatttcaca	gtgtgtttgt	gattgtttgc	tctgagagtt	cccctgtccc	2573
ctcccccttc	cctcacaccg	cgtctggtga	caaccgagtg	gctgtcatca	gcctgtgtag	2633
gcagtcattg	caccaaagcc	accagactga	caaagtgtga	tcggatgctt	ttgttcaggg	2693

ctgtgatcgg cctggggaaa taataaagat gctcttttaa aaggt 2738

<210> 81  
<211> 1085  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (329) ... (625)

<400> 81  
ggtttctatt gacttgggtt aatcgtgtga ccgcggtggc tggcacgaaa ttgaccaacc 60  
ctgggggttag tatagcttag ttaaactttc gtttattgct aaagggttaat cactgctgtt 120  
tccccgtggg gtgtggctag gctaagcgtt ttgagctgca ttgctgcgtg cttgatgctt 180  
gtcccttttg atcgtgggtga tttagagggt gaactcactg gaatggggat gcttgcattg 240  
gtaatcttac taagagctaa tagaaaggct aggaccaaac cagaaacctc caattctcat 300  
gtggaagccc atgccctcac cctccaac atg aaa gcc tct gca gca ctt ctg 352  
Met Lys Ala Ser Ala Ala Leu Leu  
1 5

tgt ctg ctg ctc aca gca gct gct ttc agc ccc cag ggg ctt gct cag 400  
Cys Leu Leu Leu Thr Ala Ala Ala Phe Ser Pro Gln Gly Leu Ala Gln  
10 15 20

cca gtt ggg att aat act tca act acc tgc tgc tac aga ttt atc aat 448  
Pro Val Gly Ile Asn Thr Ser Thr Thr Cys Cys Tyr Arg Phe Ile Asn  
25 30 35 40

aag aaa atc cct aag cag agg ctg gag agc tac aga agg acc acc agt 496  
Lys Lys Ile Pro Lys Gln Arg Leu Glu Ser Tyr Arg Arg Thr Thr Ser  
45 50 55

agc cac tgt ccc cgg gaa gct gta atc ttc aag acc aaa ctg gac aag 544  
Ser His Cys Pro Arg Glu Ala Val Ile Phe Lys Thr Lys Leu Asp Lys  
60 65 70

gag atc tgt gct gac ccc aca cag aag tgg gtc cag gac ttt atg aag 592  
Glu Ile Cys Ala Asp Pro Thr Gln Lys Trp Val Gln Asp Phe Met Lys  
75 80 85

cac ctg gac aag aaa acc caa act cca aag ctt tgaacattca tgactgaact 645  
His Leu Asp Lys Lys Thr Gln Thr Pro Lys Leu  
90 95

gaaaacaagc catgacttga gaaacaaata atttgtatac cctgtccttt ctgagagtgg 705  
ttctgagatt attttaatct aattctaagg aatatgagct ttatgtaata atgtgaatca 765  
tggtttttct tagtagattt taaaagtatt taatatattt atttaattct ccatggattt 825  
tggtggggtt tgaacataaa gccttggtat tatatgtcat ctgagtgctg taaaaactgt 885  
gggatgctcc tcccttctct acctcatggg ggtattgtat aagtccttgc aagaatcagt 945  
gcaaagattt gctttaattg ttaagatatg atgtccctat ggaagcatat tggtattata 1005  
taattacata tttgcatatg tatgactccc aaattttcac ataaaataga tttttgtata 1065  
acaaaaaaaa aaaaaaaaaa 1085

<210> 82  
<211> 775  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (84) ... (359)

```

<400> 82
aaggacacgg gcagcagaca gtggtcagtc ctttcttggc tctgctgaca ctcgagccca      60
cattccgtca cctgctcaga atc atg cag gtc tcc act gct gcc ctt gct gtc      113
               Met Gln Val Ser Thr Ala Ala Leu Ala Val
                   1                   5                   10

ctc ctc tgc acc atg gct ctc tgc aac cag ttc tct gca tca ctt gct      161
Leu Leu Cys Thr Met Ala Leu Cys Asn Gln Phe Ser Ala Ser Leu Ala
                   15                   20                   25

gct gac acg ccg acc gcc tgc tgc ttc agc tac acc tcc cgg cag att      209
Ala Asp Thr Pro Thr Ala Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile
                   30                   35                   40

cca cag aat ttc ata gct gac tac ttt gag acg agc agc cag tgc tcc      257
Pro Gln Asn Phe Ile Ala Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser
                   45                   50                   55

aag ccc ggt gtc atc ttc cta acc aag cga agc cgg cag gtc tgt gct      305
Lys Pro Gly Val Ile Phe Leu Thr Lys Arg Ser Arg Gln Val Cys Ala
                   60                   65                   70

gac ccc agt gag gag tgg gtc cag aaa tat gtc agc gac ctg gag ctg      353
Asp Pro Ser Glu Glu Trp Val Gln Lys Tyr Val Ser Asp Leu Glu Leu
                   75                   80                   85                   90

agt gcc tgaggggtcc agaagcttcg aggcccagcg acctcgggtgg gcccagtgagg      409
Ser Ala

gaggagcagg agcctgagcc ttgggaacat gcgtgtgacc tccacagcta cctcttctat      469
ggactggttg ttgccaaaca gccacactgt gggactcttc ttaacttaaa ttttaattta      529
tttatactat ttagtttttg taatttattt tcgatttcac agtgtgtttg tgattgtttg      589
ctctgagagt tcccctgtcc cctccccctt ccctcacacc gcgtctggtg acaaccgagt      649
ggctgtcatc agcctgtgta ggcagtcatg gcaccaaagc caccagactg acaaatgtgt      709
atcggatgct .tttgttcagg gctgtgatcg gcctggggaa ataataaaga tgctctttta      769
aaaggt      775

<210> 83
<211> 98
<212> PRT
<213> Homo sapiens

<400> 83
Met Lys Val Ser Ala Val Leu Leu Cys Leu Leu Leu Met Thr Ala Ala
 1                   5                   10                   15
Phe Asn Pro Gln Gly Leu Ala Gln Pro Asp Ala Leu Asn Val Pro Ser
                   20                   25                   30
Thr Cys Cys Phe Thr Phe Ser Ser Lys Lys Ile Ser Leu Gln Arg Leu
                   35                   40                   45
Lys Ser Tyr Val Ile Thr Thr Ser Ser Arg Cys Pro Gln Lys Ala Val Ile
                   50                   55                   60
Phe Arg Thr Lys Leu Gly Lys Glu Ile Cys Ala Asp Pro Lys Glu Lys
                   65                   70                   75                   80
Trp Val Gln Asn Tyr Met Lys His Leu Gly Arg Lys Ala His Thr Leu
                   85                   90                   95
Lys Thr

```

<210> 84  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A synthetic chemokine peptide variant

<400> 84  
Leu Asp Pro Lys Gln Lys Trp Ile Gln Cys  
1 5 10

<210> 85  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 85  
Trp Val Gln Cys  
1

<210> 86  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A synthetic chemokine peptide variant

<400> 86  
Trp Ile Gln Cys  
1

<210> 87  
<211> 10  
<212> PRT  
<213> Homo sapiens

<400> 87  
Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys  
1 5 10

<210> 88  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 88  
Cys Pro Lys Glu Ala Val  
1 5

<210> 89  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 89  
Ser Tyr Arg Arg Ile  
1 5

<210> 90  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 90  
Thr Ser Ser Lys Cys  
1 5

<210> 91  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 91  
Asp Tyr Phe Glu Thr Ser Ser Gln Cys  
1 5

<210> 92  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 92  
Cys Ser Lys Pro Gly Val  
1 5

<210> 93  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A synthetic chemokine peptide variant

<400> 93  
Cys Ser Tyr Arg Arg Ile Thr Ser Ser Lys Ser Pro Lys Glu Ala Val  
1 5 10 15  
Cys

<210> 94  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 94  
Ser Tyr Arg Arg Ile Thr Ser Ser Lys  
1 5

<210> 95  
<211> 11  
<212> PRT  
<213> Homo sapiens

<400> 95  
Cys Gln Val Trp Lys Gln Lys Pro Asp Ala Cys  
1 5 10

<210> 96  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 96  
Lys Lys Phe Lys  
1

<210> 97  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 97  
Arg Lys Pro Lys  
1

<210> 98  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 98  
Lys Arg Phe Lys  
1

<210> 99  
<211> 13  
<212> PRT  
<213> Homo sapiens

<400> 99  
Leu Tyr Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp  
1 5 10

<210> 100  
<211> 11  
<212> PRT  
<213> Homo sapiens

<400> 100  
His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys  
1 5 10



<210> 101  
<211> 7  
<212> PRT  
<213> Homo sapiens

<400> 101  
Val Tyr Tyr Val Gly Arg Lys  
1 5

<210> 102  
<211> 13  
<212> PRT  
<213> Homo sapiens

<400> 102  
Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys  
1 5 10

<210> 103  
<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 103  
His Leu Lys Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val  
1 5 10 15

<210> 104  
<211> 23  
<212> PRT  
<213> Homo sapiens

<400> 104  
Tyr Asn Phe Thr Asn Arg Lys Ile Ser Val Gln Arg Leu Ala Ser Tyr  
1 5 10 15  
Arg Arg Ile Thr Ser Ser Lys  
20

<210> 105  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A synthetic chemokine peptide variant

<400> 105  
Ser Tyr Arg Arg Ile Thr Ser Ser Lys Ser Pro Lys Glu Ala Val  
1 5 10 15

<210> 106  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A synthetic peptide

<400> 106  
Cys Glu Ile Cys Leu Asp Pro Lys Gln Lys Trp Ile Gln Cys  
1 5 10

<210> 107  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A synthetic peptide

<400> 107  
Cys Trp Val Gln Cys  
1 5

<210> 108  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A synthetic peptide

<400> 108  
Cys Lys Gln Lys Trp Val Gln Cys  
1 5

<210> 109  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A synthetic peptide

<400> 109  
Cys Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Pro Lys Glu Ala Val  
1 5 10 15  
Cys

<210> 110  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A synthetic peptide

<400> 110  
Cys His Leu Lys Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val  
1 5 10 15  
Cys

<210> 111  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A synthetic peptide

<400> 111  
Cys Ser Tyr Arg Arg Ile Thr Ser Ser Lys Ser Pro Lys Glu Ala Val  
1 5 10 15  
Cys